

FIG. 1

Enzymes : 36 of 538 enzymes (Filtered)

Settings : Circular, Certain Sites Only, Standard Genetic Code

PstI

GAAACCAGCAGCGGCTATCCGCGCATCCATGCCCCGAAGTGCAGGAGTGGGGAGGCACGATGGCCGCTTTGGTCGAGGC
CTTTGGTCGTCGCCGATAGGCGCGTAGGTACGGGGGCTTGACGTCCTCACCCCTCCGTGCTACCGGCGAAACCAGCTCCG 2800

BamHI

GGATCCTAGCAGAAAAATAAGACTTGATTCCCCCTTAAAATTACAACTGCTAGAAAATGAATGGCTCTCCCGCCTTTTTT
CCTAGGATCGTCTTTTTATTCTGAAGTAAGGGGAATTTTAAATGTTGACGATCTTTTACTTACCGAGAGGGCGGAAAAAA 2880

BLV Promoter

NarI

PvuII

GAGGGGGAATCATTTGTATGAAAGATCATGCCGACCTAGGCGCCGCCACCGCCCCGTAAACCAGACAGAGACGTCAGCTG
CTCCCCCTTAGTAAACATACTTTCTAGTACGGCTGGATCCGCGGCGGTGGCGGGGCATTGGTCTGTCTCTGCAGTCGAC 2960

BLV Promoter

PvuII

CCAGAAAAGCTGGTGACGGCAGCTGGTGGCTAGAATCCCCGTACCTCCCCAACTTCCCCTTTCCCGAAAAATCCACACCC
GGTCTTTTCGACCACTGCCGTCGACCACCGATCTTAGGGGCATGGAGGGGTGAAGGGGAAAGGGCTTTTAGGTGTGGG 3040

BLV Promoter

NaeI

TGAGCTGCTGACCTCACCTGCTGATAAATTAATAAAATGCCGGCCCTGTGAGTTAGCGGCACCAGAAGCGTTCTTCTCC
ACTCGACGACTGGAGTGGACGACTATTTAATTATTTTACGGCCGGGACAGCTCAATCGCCGTGGTCTTCGAAGAAGAGG 3120

BLV Promoter

XhoI

HindIII

TGAGACCCTCGTGCTCAGCTCTCGGTCTGCCTCGAGAAGCTTGTATCACAAGTTTGTACAAAAAGCTGAACGAGAAA
ACTCTGGGAGCACGAGTCGAGAGCCAGGACGGAGCTCTTCAACAATAGTGTTCAAACATGTTTTTCGACTTGCTCTTT 3200

BLV Promoter

Gateway

att R1

FIG. 2

SEQUENCE LISTING -- TAX [Bovine leukemia virus]

LOCUS AAF97920 309 aa
ACCESSION AAF97920

NUCLEOTIDE SEQUENCE (SEQ ID NO:2):

ATG GCA AGT GTT GTT GGT TGG GGG CCC CAC TCT CTA CAT GCC TGC CCG
GCC CTG GTT TTG TCC AAT GAC GTC ACC ATC GAT GCC TGG TGC CCC CTC
TGC GGG CCC CAT GAG CGA CTC CAA TTC GAA AGG ATC GAC ACC ACG CAC
ACC TGC GAG ACC CAC CGT ATC ACC TGG ACC GCC GAT GGA CGA CCT TTC
GGC CTC AAT GGA GCG CTG TTC CCT CGA CTG CAT GTC TCC AGA GAC CCG
GCC CCA AGG GCC CGA CGA CTC TGG ATC AAC TGC CCC CTT CCG GCC GTT
CGC GCT CAG CCC GGC CCG GTT TCA CTT TCC CCC TTC GAG CGG TCC CCC
TTC CAG CCC TAC CAA TGC CAA TTG CCC TCG GCC TCT AGC GAC GGT TGC
CCC GTC ATC GGG CAC GGC CTT CTT CCC TGG AAC AAC TTA GTA ACG CAT
CCT TGT CCT CGG AAA GTC CTT ATA TTA AAT CAA ATG GCC AAT TTT TCC
TTA CTC CCC CCC TTC AAT ACC CTC CTT GTG GAC CCC CTC CGG TTG TCC
GTC TTT GCC CCA GAC ACC AGG GGA GCC ATA CGT TAT CTC TCC ACC CTT
TTG ACG CTA TGC CCA GCT ACT TGT ATT CTA CCC CTC GGC GA GCC CTT
CTC TCC TAA TGT CCC CAT ATG TCG CTT TCC CCG GGA CTC CAA TGA ACC
CCC CCT TTC AGA ATT CGA GCT GCC CCT TAT CCA AAC GCC CGG CCT GTC
TTG GTC TGT CCC CGC GAT CGA CCT ATT CCT AAC CGG CCC CCC TTC CCC
ATG CGA CCG GTT ACA CGT ATG GTC CAG TCC TCA GGC CTT ACA GCG CTT
CCT CCA TGA CCC TAC GCT AAC CTG GTC AGA ATT GGT TGC TAG CAG GAA
ACT AAG ACT TGA TTC ACC CTT AAA ATT ACA ACT GTT AGA AAA TGA ATG
GCT CTC CCG CCT TTT TTG

PROTEIN SEQUENCE (SEQ ID NO:7):

MASVVGWGP HSLHACPALVLSNDVTIDAWCPLCGPHERLQFERIDTTHTCETHRITW
TADGRPFGLNGALFPRLHVS RDPAPRARRLWINCP LPAVRAQPGPVSLSPFERSPF
QPYQCQLPSASSDGCPVIGHGLLPWNNLVTHPCPRKVLILNQMANFSLLPPFNTLLV
DPLRLSVFAPDTRGAIRYLSTLLTLC PATCILPLGEPFSPNPICRFPRDSNEPPLSEF
ELPLIQTPGLSWSVPAIDLFLTGPSPCDRLHVWSSPQALQRFLHDPTLTW
SELVASRKLR LDSPLKLQLLENEWLSRLF

FIG. 3

SEQUENCE LISTING -- HTLV-1 Promoter sequence (SEQ ID NO:4)

```
1  TGACAATGAC CATGAGCCCC AAATATCCCC CGGGGGGCTTA GAGCCTCTCA GTGAAAAACA
61  TTTCCGTGAA ACAGAAGTCT GAGAAGGTCA GGGCCCAGAA TAAGGCTCTG ACGTCTCCCC
121 CCGGAGGACA GCTCAGCACC AGCTCAGGCT AGGCCCTGAC GTGTCCCCCT AAAGACAAAT
181 CATAAGCTCA GACCTCCGGG AAGCCACCGG GAACCACCCA TTTCTCCCC ATGTTTGTCA
241 AGCCGTCCTC AGGCGTTGAC GACAACCCCT CACCTCAAAA AACTTTTCAT GGCACGCATA
301 CGGCTCAATA AAATAACAGG AGTCTATAAA AGCGTGGGGA CAGTTCAGGA GGG
```

FIG. 4

**SEQUENCE LISTING -- HTLV1 Tax Nucleic Acid (SEQ ID NO:3) and
Protein sequence (SEQ ID NO:8)**

1	ATG	GCC	CAC	TTC	CCA	GGG	TTT	GGA	CAG	AGT	CTT	CTT	TTC	GGA	TAC	45
1	Met	Ala	His	Phe	Pro	Gly	Phe	Gly	Gln	Ser	Leu	Leu	Phe	Gly	Tyr	15
46	CCA	GTC	TAC	GTG	TTT	GGA	GAC	TGT	GTA	CAA	GGC	GAC	TGG	TGC	CCC	90
16	Pro	Val	Tyr	Val	Phe	Gly	Asp	Cys	Val	Gln	Gly	Asp	Trp	Cys	Pro	30
91	ATC	TCT	GGG	GGA	CTA	TGT	TCG	GCC	CGC	CTA	CAT	CGT	CAC	GCC	CTA	135
31	Ile	Ser	Gly	Gly	Leu	Cys	Ser	Ala	Arg	Leu	His	Arg	His	Ala	Leu	45
136	CTG	GCC	ACC	TGT	CCA	GAG	CAT	CAG	ATC	ACC	TGG	GAC	CCC	ATT	GAT	180
46	Leu	Ala	Thr	Cys	Pro	Glu	His	Gln	Ile	Thr	Trp	Asp	Pro	Ile	Asp	60
181	GGA	CGC	GTT	ATC	GGC	TCA	GCT	CTA	CAG	TTC	CTT	ATC	CCT	CGA	CTC	225
61	Gly	Arg	Val	Ile	Gly	Ser	Ala	Leu	Gln	Phe	Leu	Ile	Pro	Arg	Leu	75
226	CCC	TCC	TTC	CCC	ACC	CAG	AGA	ACC	TCT	AAG	ACC	CTC	AAG	GTC	CTT	270
76	Pro	Ser	Phe	Pro	Thr	Gln	Arg	Thr	Ser	Lys	Thr	Leu	Lys	Val	Leu	90
271	ACC	CCG	CCA	ATC	ACT	CAT	ACA	ACC	CCC	AAC	ATT	CCA	CCC	TCC	TTC	315
91	Thr	Pro	Pro	Ile	Thr	His	Thr	Thr	Pro	Asn	Ile	Pro	Pro	Ser	Phe	105
316	CTC	CAG	GCC	ATG	CGC	AAA	TAC	TCC	CCC	TTC	CGA	AAT	GGA	TAC	ATG	360
106	Leu	Gln	Ala	Met	Arg	Lys	Tyr	Ser	Pro	Phe	Arg	Asn	Gly	Tyr	Met	120
361	GAA	CCC	ACC	CTT	GGG	CAG	CAC	CTC	CCA	ACC	CTG	TCT	TTT	CCA	GAC	405
121	Glu	Pro	Thr	Leu	Gly	Gln	His	Leu	Pro	Thr	Leu	Ser	Phe	Pro	Asp	135
406	CCC	GGA	CTC	CGG	CCC	CAA	AAC	CTG	TAC	ACC	CTC	TGG	GGA	GGC	TCC	450
136	Pro	Gly	Leu	Arg	Pro	Gln	Asn	Leu	Tyr	Thr	Leu	Trp	Gly	Gly	Ser	150
451	GTT	GTC	TGC	ATG	TAC	CTC	TAC	CAG	CTT	TCC	CCC	CCC	ATC	ACC	TGG	495
151	Val	Val	Cys	Met	Tyr	Leu	Tyr	Gln	Leu	Ser	Pro	Pro	Ile	Thr	Trp	165
496	CCC	CTC	CTG	CCC	CAC	GTG	ATT	TTT	TGC	CAC	CCC	GGC	CAG	CTC	GGG	540
166	Pro	Leu	Leu	Pro	His	Val	Ile	Phe	Cys	His	Pro	Gly	Gln	Leu	Gly	180
541	GCC	TTC	CTC	ACC	AAT	GTT	CCG	TAC	AAG	CGA	ATA	GAA	GAA	CTC	CTC	585
181	Ala	Phe	Leu	Thr	Asn	Val	Pro	Tyr	Lys	Arg	Ile	Glu	Glu	Leu	Leu	195
586	TAT	AAA	ATT	TCC	CTT	ACC	ACA	GGG	GCC	CTA	ATA	ATT	CTA	CCC	GAA	630
196	Tyr	Lys	Ile	Ser	Leu	Thr	Thr	Gly	Ala	Leu	Ile	Ile	Leu	Pro	Glu	210
631	GAC	TGT	TTG	CCC	ACC	ACC	CTT	TTC	CAG	CCT	GTT	AGG	GCA	CCC	GTC	675
211	Asp	Cys	Leu	Pro	Thr	Thr	Leu	Phe	Gln	Pro	Val	Arg	Ala	Pro	Val	225
676	ACG	CTA	ACA	GCC	TGG	CAA	AAC	GGC	CTC	CTT	CCG	TTC	CAC	TCA	ACC	720
226	Thr	Leu	Thr	Ala	Trp	Gln	Asn	Gly	Leu	Leu	Pro	Phe	His	Ser	Thr	240
721	CTC	ACC	ACT	CCA	GGC	CTT	ATT	TGG	ACA	TTT	ACC	GAT	GGC	ACG	CCT	765
241	Leu	Thr	Thr	Pro	Gly	Leu	Ile	Trp	Thr	Phe	Thr	Asp	Gly	Thr	Pro	255

FIG. 5

766	ATG	ATT	TCC	GGG	CCC	TGC	CCT	AAA	GAT	GGC	CAG	CCA	TCT	TTA	GTA	810
256	Met	Ile	Ser	Gly	Pro	Cys	Pro	Lys	Asp	Gly	Gln	Pro	Ser	Leu	Val	270
811	CTA	CAG	TCC	TCC	TCC	TTT	ATA	TTT	CAC	AAA	TTT	CAA	ACC	AAG	GCC	855
271	Leu	Gln	Ser	Ser	Ser	Phe	Ile	Phe	His	Lys	Phe	Gln	Thr	Lys	Ala	285
856	TAC	CAC	CCC	TCA	TTT	CTA	CTC	TCA	CAC	GGC	CTC	ATA	CAG	TAC	TCT	900
286	Tyr	His	Pro	Ser	Phe	Leu	Leu	Ser	His	Gly	Leu	Ile	Gln	Tyr	Ser	300
901	TCC	TTT	CAT	AAT	TTA	CAT	CTC	CTG	TTT	GAA	GAA	TAC	ACC	AAC	ATC	945
301	Ser	Phe	His	Asn	Leu	His	Leu	Leu	Phe	Glu	Glu	Tyr	Thr	Asn	Ile	315
946	CCC	ATT	TCT	CTA	CTT	TTT	AAC	GAA	AAA	GAG	GCA	GAT	GAC	AAT	GAC	990
316	Pro	Ile	Ser	Leu	Leu	Phe	Asn	Glu	Lys	Glu	Ala	Asp	Asp	Asn	Asp	330
991	CAT	GAG	CCC	CAA	ATA	TCC	CCC	GGG	GGC	TTA	GAG	CCT	CCC	AGT	GAA	1035
331	His	Glu	Pro	Gln	Ile	Ser	Pro	Gly	Gly	Leu	Glu	Pro	Pro	Ser	Glu	345
1036	AAA	CAT	TTC	CGC	GAA	ACA	GAA	GTC	TGA							1070
346	Lys	His	Phe	Arg	Glu	Thr	Glu	Val	TRM							354

FIG. 5 (Cont.)

SEQUENCE LISTING -- HIV Promoter sequence (SEQ ID NO:5)

1	CTGGAAGGGC	TAATTTGGTC	CCAAAGAAGA	CAAGAGATCC	TTGATCTGTG	GATCTACCAC
61	ACACAAGGCT	ACTTCCCTGA	TTGGCAGAAT	TACACACCAG	GGCCAGGGAT	CAGATATCCA
121	CTGACCTTTG	GATGGTGCTT	CAAGCTAGTA	CCAGTTGAGC	CAGAGAAGGT	AGAAGAGGCC
181	AATGAAGGAG	AGAACAACAG	CTTGTTACAC	CCTATGAGCC	TGCATGGGAT	GGAGGACGCG
241	GAGAAAGAAG	TGTTAGTGTG	GAGGTTTGAC	AGCAAAC TAG	CATTTTCATCA	CATGGCCCCGA
301	GAGCTGCATC	CGGAGTACTA	CAAAGACTGC	TGACATCGAG	CTTTCTACAA	GGGACTTTCC
361	GCTGGGGACT	TTCCAGGGAG	GCGTGGCCTG	GGCGGGACTG	GGGAGTGGCG	TCCCTCAGAT
421	GCTGCATATA	AGCAGCTGCT	TTTTGCCTGT	ACTGGG		

FIG. 6

**SEQUENCE LISTING -- HIV Tat nucleic acid (SEQ ID NO:6) and amino
acid (SEQ ID NO:9) of HIV Tat.**

1	ATG GAG CCA GTA GAT CCT AAT CTA GAG CCC TGG AAG CAT CCA GGA	45
1	Met Glu Pro Val Asp Pro Asn Leu Glu Pro Trp Lys His Pro Gly	15
46	AGT CAG CCT AGG ACT GCT TGT AAC AAT TGC TAT TGT AAA AAG TGT	90
16	Ser Gln Pro Arg Thr Ala Cys Asn Asn Cys Tyr Cys Lys Lys Cys	30
91	TGC TTT CAT TGC TAC GCG TGT TTC ACA AGA AAA GGC TTA GGC ATC	135
31	Cys Phe His Cys Tyr Ala Cys Phe Thr Arg Lys Gly Leu Gly Ile	45
136	TCC TAT GGC AGG AAG AAG CGG AGA CAG CGA CGA AGA GCT CCT CAG	180
46	Ser Tyr Gly Arg Lys Lys Arg Arg Gln Arg Arg Arg Ala Pro Gln	60
181	GAC AGT CAG ACT CAT CAA GCT TCT CTA TCA AAG CAA CCC GCC TCC	225
61	Asp Ser Gln Thr His Gln Ala Ser Leu Ser Lys Gln Pro Ala Ser	75
226	CAG TCC CGA GGG GAC CCG ACA GGC CCG ACG GAA TCG AAG AAG AAG	270
76	Gln Ser Arg Gly Asp Pro Thr Gly Pro Thr Glu Ser Lys Lys Lys	90
271	GTG GAG AGA GAG ACA GAG ACA GAT CCG TTC GAT TAG	306
91	Val Glu Arg Glu Thr Glu Thr Asp Pro Phe Asp TRM	102

FIG. 7

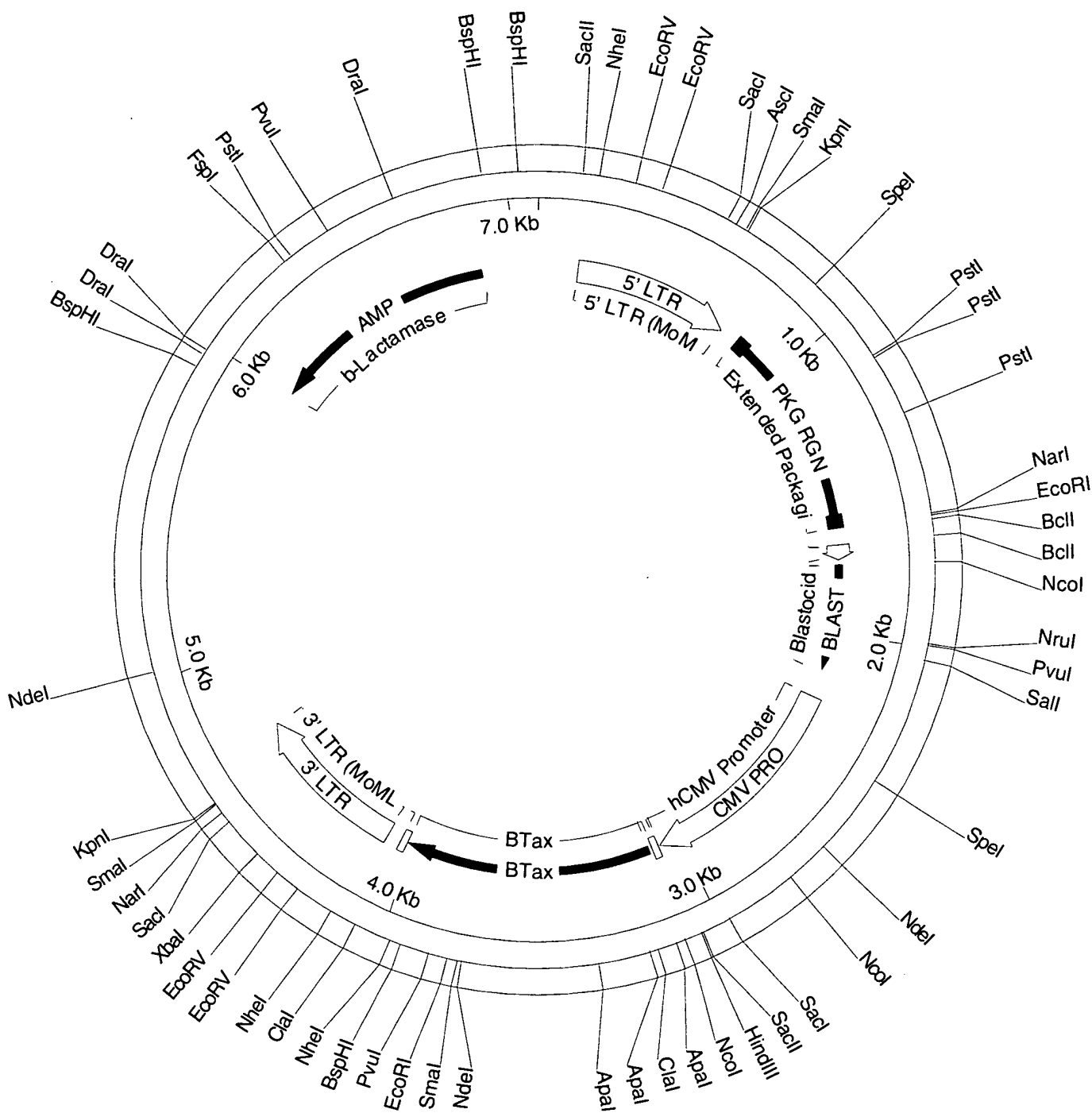


FIG. 8

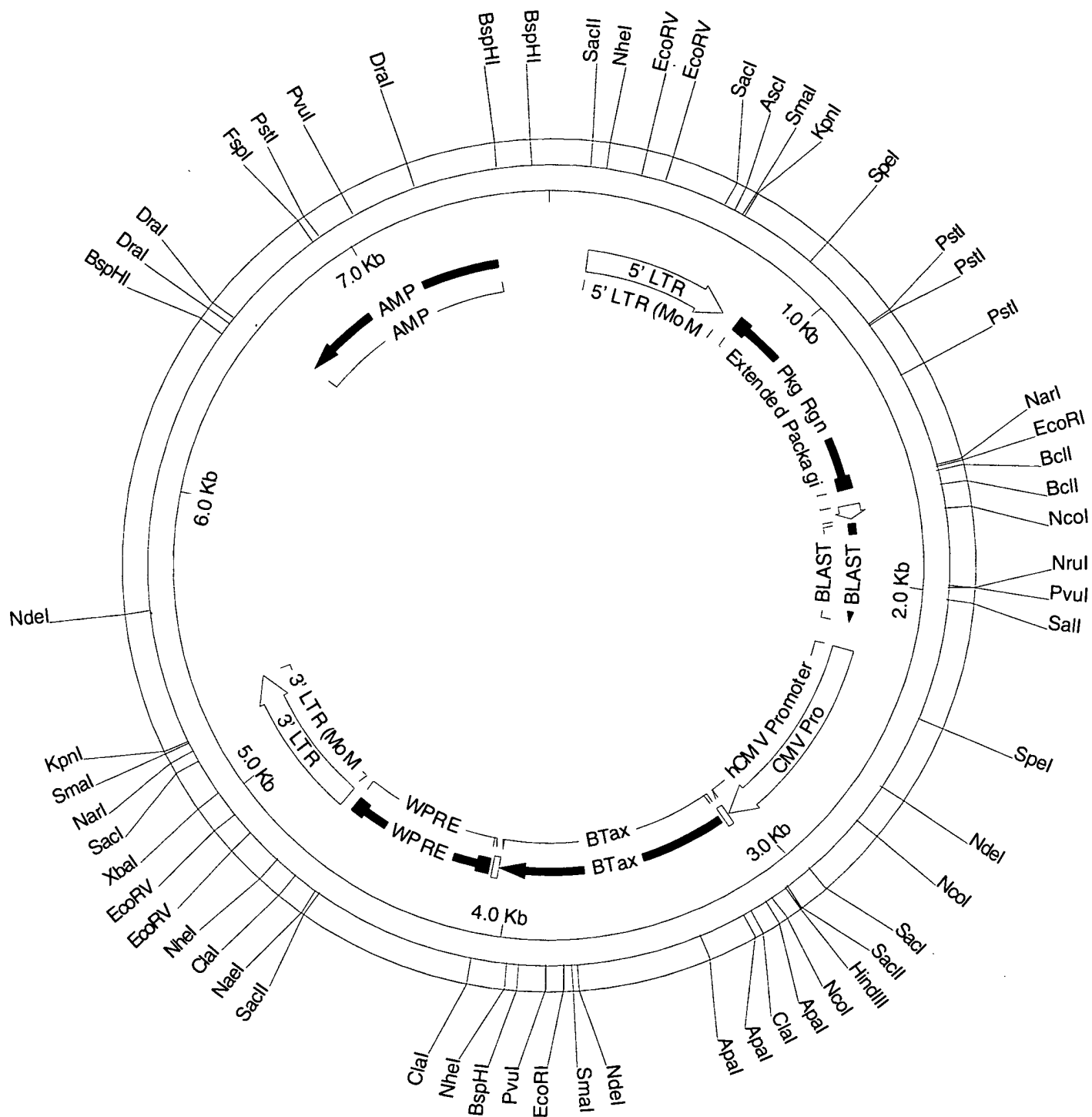


FIG. 9

FIG. 10

Page 1

Friday, November 15, 2002 12:30 PM

pLBC-BTaxW Map.MPD (1 > 7685) Site and Sequence

Enzymes : 35 of 538 enzymes (Filtered)

Settings : Circular, Certain Sites Only, Standard Genetic Code

GAATTAATTCATACCAGATCACCGAAAACGTGCTCTCAAATGTGTCCCTCACACTCCCAAATTCGCGGGCTTCTGCCT
CTTAATTAAGTATGGTCTAGTGGCTTTTGACAGGAGGTTTACACAGGGGAGTGTGAGGGTTTAAGCGCCGAAGACGGA

SacII

CTTAGACCACTCTACCCTATTCCCCACACTCACCGGAGCCAAAGCCGCGGCCCTTCCGTTTCTTTGCTTTTGAAGACCC
GAATCTGGTGAGATGGGATAAGGGGTGTGAGTGGCCTCGGTTTCGGCGCCGGAAGGCAAGAAACGAAAACCTTCTGGG

5' LTR

5' LTR (MoMS-

NheI

CACCCGTAGGTGGCAAGCTAGCTTAAGTAACGCCACTTTGCAAGGCATGGAAAAATACATAACTGAGAATAGAAAAGTTC
GTGGGCATCCACCGTTCGATCGAATTCATTGCGGTGAAACGTTCCGTACCTTTTTATGTATTGACTCTTATCTTTTCAAG

5' LTR

5' LTR (MoMSV)

EcoRV

AGATCAAGGTCAGGAACAAAGAAACAGCTGAATACCAACAGGATATCTGTGGTAAGCGGTTCTTGCCCCGGCTCAGGGC
TCTAGTTCCAGTCTTGTCTTTGTGCGACTTATGGTTTGTCTATAGACACCATTCGCCAAGGACGGGGCCGAGTCCCG

5' LTR

5' LTR (MoMSV)

EcoRV

CAAGAACAGATGAGACAGCTGAGTGATGGGCCAAACAGGATATCTGTGGTAAGCAGTTCTTGCCCCGGCTCGGGGCCAAG
GTTCTTGTCTACTCTGTGCGACTCACTACCCGGTTTGTCTATAGACACCATTCGTCAAGGACGGGGCCGAGCCCCGGTTC

5' LTR

5' LTR (MoMSV)

AACAGATGGTCCCCAGATGCGGTCCAGCCCTCAGCAGTTTCTAGTGAATCATCAGATGTTTCCAGGGTGCCCCAAGGACC
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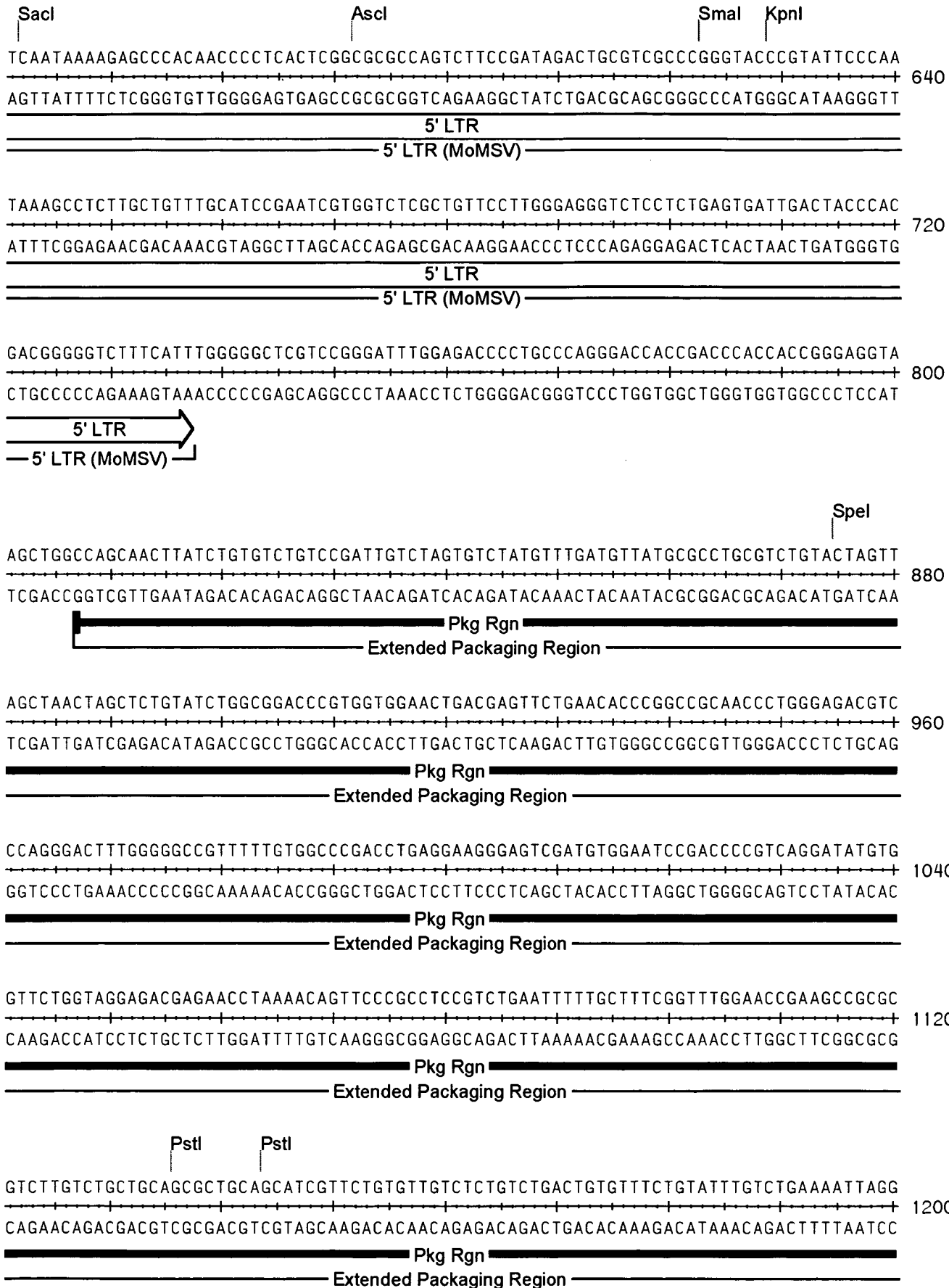
5' LTR

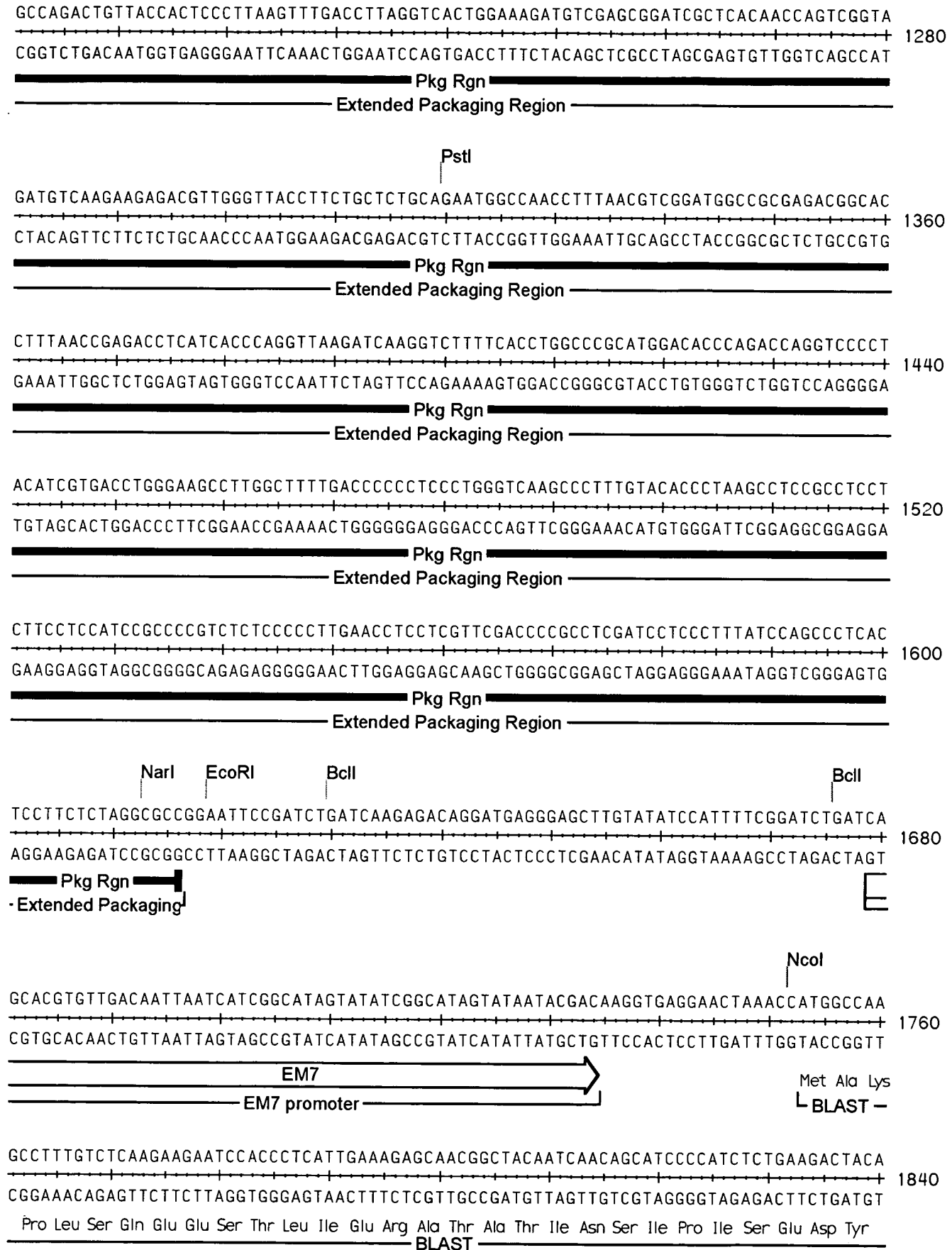
5' LTR (MoMSV)

TGAAAATGACCCTGTACCTTATTTGAACTAACCAATCAGTTCGCTTCTCGCTTCTGTTTCGCGCGCTTCCGCTCTCCGAGC
ACTTTTACTGGGACATGGAATAAACTTGATTGGTTAGTCAAGCGAAGAGCGAAGACAAGCGCGCAAGGCGAGAGGCTCG

5' LTR

5' LTR (MoMSV)





Friday, November 15, 2002 12:30 PM
pLBC-BTaxW Map.MPD (1 > 7685) Site and Sequence

CGCTCGCCAGCGCAGCTCTCTAGCGACGGCCGCATCTTCACTGGTGTCAATGTATATCATTTTACTGGGGGACCTTGT
1920
CGCAGCGGTTCGCTCGAGAGAGATCGCTGCCGGCGTAGAAGTGACCACAGTTACATATAGTAAAATGACCCCTGGAACA
Ser Val Ala Ser Ala Ala Leu Ser Ser Asp Gly Arg Ile Phe Thr Gly Val Asn Val Tyr His Phe Thr Gly Gly Pro Cys
BLAST

CGAGAACTCGTGGTGTGGGCACTGCTGCTGCTGCGGCAGCTGGCAACCTGACTTGTATCGTCGCGATCGGAAATGAGAA
2000
CGTCTTGAGCACCACGACCCGTGACGACGACGACGCCGTGACCGTTGGACTGAACATAGCAGCGCTAGCCTTTACTCTT
Ala Glu Leu Val Val Leu Gly Thr Ala Ala Ala Ala Ala Gly Asn Leu Thr Cys Ile Val Ala Ile Gly Asn Glu Asn
BLAST

CAGGGGCATCTTGAGCCCTGCGGACGGTGTGACAGGTGCTTCTCGATCTGCATCCTGGGATCAAAGCGATAGTGAAGG
2080
GTCCCGTAGAACTCGGGACGCTGCCACAGCTGTCCACGAAGAGCTAGACGTAGGACCCTAGTTTCGTATCACTTCC
Arg Gly Ile Leu Ser Pro Cys Gly Arg Cys Arg Gln Val Leu Leu Asp Leu His Pro Gly Ile Lys Ala Ile Val Lys
BLAST

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2160
TGCTACTACCTGTCGGCTGCCGTCAACCCTAAGCACTTAACGACGGGAGACCAATACACACCCTCCCGATTTCGTGAAGCA
Asp Ser Asp Gly Gln Pro Thr Ala Val Gly Ile Arg Glu Leu Leu Pro Ser Gly Tyr Val Trp Glu Gly
BLAST

GGCCGAGGAGCAGGACTGACACGTGCTACGAGATTTTCGATTCCACCGCCGCTTCTATGAAAGGTTGGGCTTCGGAATCG
2240
CCGGCTCCTCGTCTGACTGTGCACGATGCTCTAAAGCTAAGGTGGCGGCGGAAGATACTTTCCAACCCGAAGCCTTAGC

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CMV Pro
hCMV Promoter

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2400
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CMV Pro
hCMV Promoter

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2480
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CMV Pro
hCMV Promoter

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CATTACCGGGCGGACCGACTGGCGGGTTGCTGGGGGCGGGTAACTGCAGTTATTACTGCATACAAGGGTATCATTGCGG

CMV Pro

hCMV Promoter

NdeI

AATAGGGACTTTCATTGACGTCAATGGGTGGAGTATTTACGGTAACTGCCCACTTGGCAGTACATCAAGTGTATCATA 2640
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CMV Pro

hCMV Promoter

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CMV Pro

hCMV Promoter

NcoI

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CMV Pro

hCMV Promoter

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CMV Pro

hCMV Promoter

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CMV Pro

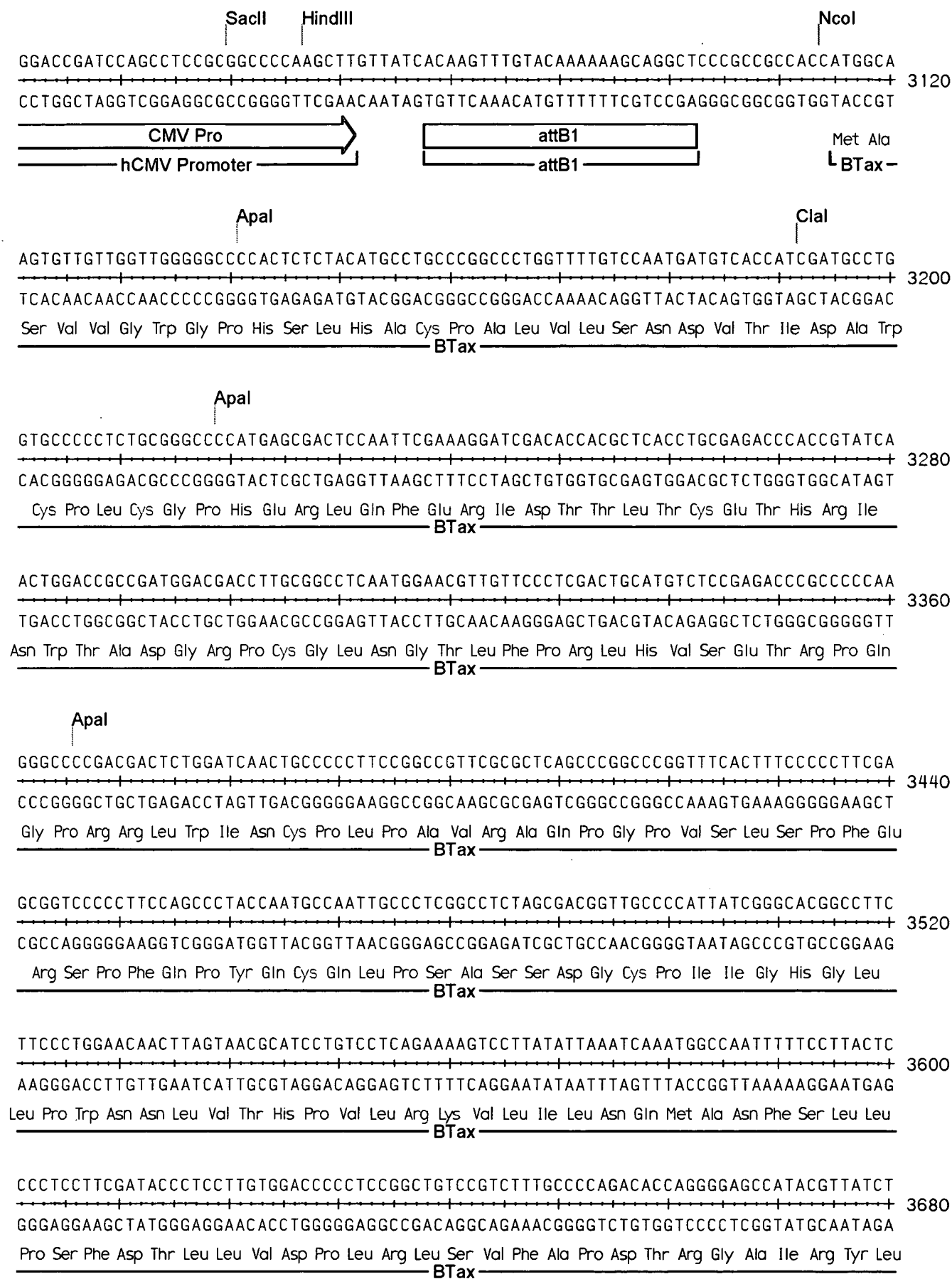
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SacI

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CMV Pro

hCMV Promoter



NdeI

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GAGGTGGGAAACTGCGATACGGCCGATGAACATAAGATGGGGATCCGCTCGGGAAGAGAGGATTACAGGGGTATACGG
Ser Thr Leu Leu Thr Leu Cys Pro Ala Thr Cys Ile Leu Pro Leu Gly Glu Pro Phe Ser Pro Asn Val Pro Ile Cys
BTax

SmaI EcoRI

GCTTTCCCCGGGACTCCAATGAACCCCCCTTTTCTCAGATTGAGCTGCCCTTATCCAACGCCCGGCCTGTCTTGGTCT 3840
CGAAAGGGGCCCTGAGGTTACTTGGGGGGAAAGTCTTAAGCTCGACGGGGAATAGGTTTGGGGCCGGACAGAACCAGA
Arg Phe Pro Arg Asp Ser Asn Glu Pro Pro Leu Ser Glu Phe Glu Leu Pro Leu Ile Gln Thr Pro Gly Leu Ser Trp Ser
BTax

PvuI

GTCCCCGCGATCGACCTATTCCTAACCGGTCCCCCTTCCCATGCGACCGGTTACACGTATGGTCCAGTCCTCAGGCCTT 3920
CAGGGGCGCTAGCTGGATAAGGATTGGCCAGGGGGAAGGGGTACGCTGGCCAATGTGCATACCAGGTCAGGAGTCCGGAA
Val Pro Ala Ile Asp Leu Phe Leu Thr Gly Pro Pro Ser Pro Cys Asp Arg Leu His Val Trp Ser Ser Pro Gln Ala Leu
BTax

BspHI NheI

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TGTCGCGAAGGAAGTACTGGGATGCGATTGGACCAGGCTTAATCAACGATCGTCTTTTATTCTGAACTAAGGGGAATT
Gln Arg Phe Leu His Asp Pro Thr Leu Thr Trp Ser Glu Leu Val Ala Ser Arg Lys Ile Arg Leu Asp Ser Pro Leu
BTax

ClaI

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Lys Leu Gln Leu Leu Glu Asn Glu Trp Leu Ser Arg Leu Phe attB2
BTax

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WPRE
WPRE

SacII NaeI
TCAATCCAGCGGACCTTCCTTCCCGCGGCCTGCTGCCGGCTCTGCGGCCTCTTCCGCGTCTTCGCCTTCGCCCTCAGACG 4640
AGTTAGGTCGCCTGGAAGGAAGGGCGCCGGACGACGGCCGAGACGCCGGAGAAGGCGCAGAAGCGGAAGCGGGAGTCTGC
WPRE
WPRE

Clal
AGTCGGATCTCCCTTTGGGCCGCTCCCCGCTGATCGATAAAATAAAAGATTTTATTTAGTCTCCAGAAAAAGGGGGGA 4720
TCAGCCTAGAGGGAAACCGCGGAGGGGCGGACTAGCTATTTTATTTCTAAAATAAATCAGAGGTCTTTTCCCCCT
WPRE
WPRE

NheI
ATGAAAGACCCACCTGTAGGTTTGGCAAGCTAGCTTAAGTAACGCCATTTTGAAGGCATGGAAAAATACATAACTGAG 4800
TACTTTCTGGGGTGGACATCAAACCGTTCGATCGAATTCATTGCGGTAAACGTTCCGTACCTTTTATGTATTGACTC
3' LTR
3' LTR (MoMLV)

EcoRV

AATAGAGAAGTTCAGATCAAGGTCAGGAACAGATGGAACAGCTGAATATGGGCCAAACAGGATATCTGTGGTAAGCAGTT 4880
TTATCTCTTCAAGTCTAGTTCAGTCCCTTGTCTACCTTGTGCACTTATACCCGGTTTGTCTATAGACACCATTTCGTCAA

3' LTR

3' LTR (MoMLV)

EcoRV

CCTGCCCCGGCTCAGGGCCAAGAACAGATGGAACAGCTGAATATGGGCCAAACAGGATATCTGTGGTAAGCAGTTCCTGC 4960
GGACGGGGCCGAGTCCCGTTCTTGTCTACCTTGTGCACTTATACCCGGTTTGTCTATAGACACCATTTCGTCAAGGACG

3' LTR

3' LTR (MoMLV)

XbaI

CCCGGCTCAGGGCCAAGAACAGATGGTCCCCAGATGCGGTCCAGCCCTCAGCAGTTTCTAGAGAACCATCAGATGTTTCC 5040
GGGCCGAGTCCCGTTCTTGTCTACCAGGGGTCTACGCCAGGTCGGGAGTCGTCAAAGATCTCTTGGTAGTCTACAAAGG

3' LTR

3' LTR (MoMLV)

AGGGTGCCCCAAGGACCTGAAATGACCCTGTGCCTTATTTGAACTAACCAATCAGTTCGCTTCTCGCTTCTGTTTCGCGCG 5120
TCCCACGGGGTTCTGGACTTTACTGGGACACGGAATAAACTTGATTGGTTAGTCAAGCGAAGAGCGAAGACAAGCGCGC

3' LTR

3' LTR (MoMLV)

SacI

NarI

SmaI

CTTCTGCTCCCCGAGCTCAATAAAAGAGCCCACAACCCCTCACTCGGGGCGCCAGTCTCCGATTGACTGAGTCGCCCGG 5200
GAAGACGAGGGGCTCGAGTTATTTCTCGGGTGTGGGGAGTGAGCCCCGCGGTCAGGAGGCTAACTGACTCAGCGGGCC

3' LTR

3' LTR (MoMLV)

KpnI

GTACCCGTGTATCCAATAAACCCCTTGCAGTTGCATCCGACTTGTGGTCTCGCTGTTCCCTTGGGAGGGTCTCCTCTGAG 5280
CATGGGCACATAGGTTATTTGGGAGAACGTCAACGTAGGCTGAACACCAGAGCGACAAGGAACCCCTCCAGAGGAGACTC

3' LTR

3' LTR (MoMLV)

TGATTGACTACCCGTCAGCGGGGGTCTTTTCATTTTCCATTGGGGGCTCGTCCGGGATCGGGAGACCCCTGCCAGGGAC 5360
ACTAACTGATGGGCAGTCGCCCCAGAAAGTAAAAAGGTAACCCCCGAGCAGGCCCTAGCCCTCTGGGGACGGGTCCCTG

3' LTR

3' LTR (MoMLV)

CACCGACCCACCACCGGGAGGTAAGCTGGCTGCCTCGCGCGTTTCGGTGATGACGGTGAAAACCTCTGACACATGCAGCT
5440
GTGGCTGGGTGGTGGCCCTCCATTTCGACCGACGGAGCGCGCAAAGCCACTACTGCCACTTTTGGAGACTGTGTACGTCTGA

CCCGGAGACGGTCACAGCTTGTCTGTAAGCGGATGCCGGGAGCAGACAAGCCCGTCAGGGCGCGTCAGCGGGTGTGGCG
5520
GGGCCTCTGCCAGTGTGCAACAGACATTTCGCTACGGCCCTCGTCTGTTTCGGGCAGTCCCAGCGCAGTCGCCACAACCGC

GGTGTGGGGCGCAGCCATGACCCAGTCACGTAGCGATAGCGGAGTGATACTGGCTTAATACTATGCGGCATCAGAGCAGA
5600
CCACAGCCCCGCGTCGGTACTGGGTCAGTGCATCGCTATCGCTCACATATGACCGAATTGATACGCCGTAGTCTCGTCT

NdeI
TTGTAAGTGCACCATATGCGGTGTGAAATACCGCACAGATGCGTAAGGAGAAAAATACCGCATCAGGCGCTCTTCC
5680
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GCTTCCTCGCTCACTGACTCGCTGCGCTCGGTGCTTCGGCTGCGGCGAGCGGTATCAGCTCACTCAAAGGCGGTAATACG
5760
CGAAGGAGCGAGTGACTGAGCGACGCGAGCCAGCAAGCCGACGCCGCTCGCCATAGTCGAGTGAGTTTCCGCCATTATGC

GTTATCCACAGAATCAGGGGATAACGCAGGAAAGAACATGTGAGCAAAAGGCCAGCAAAAGGCCAGGAACCGTAAAAAGG
5840
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CCGCGTTGCTGGCGTTTTTCCATAGGCTCCGCCCCCTGACGAGCATCACAAAAATCGACGCTCAAGTCAGAGGTGGCGA
5920
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AACCCGACAGGACTATAAAGATACCAGGCGTTTCCCCCTGGAAGCTCCCTCGTGCGCTCTCCTGTTCCGACCCTGCCGCT
6000
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TACCGGATACCTGTCCGCCTTTCTCCCTTCGGGAAGCGTGCGCTTTTCTCATAGCTCACGCTGTAGGTATCTCAGTTCCG
6080
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TGTAGGTGTTTCGCTCCAAGCTGGGCTGTGTGCACGAACCCCCGTTAGCCCGACCGCTGCGCCTTATCCGGTAACTAT
6160
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CGTCTTGAGTCCAACCCGGTAAGACACGACTTATCGCCACTGGCAGCAGCCACTGGTAACAGGATTAGCAGAGCGAGGTA
6240
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TGTAGGCGGTGCTACAGAGTTCTTGAAGTGGTGGCCTAACTACGGCTACACTAGAAGGACAGTATTTGGTATCTGCGCTC
6320
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TGCTGAAGCCAGTTACCTTCGGAAAAAGAGTTGGTAGCTCTTGATCCGGCAAACAAACCACCGCTGGTAGCGGTGGTTTT
6400
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TTTGTGTTGCAAGCAGCAGATTACGCGCAGAAAAAAGGATCTCAAGAAGATCCTTTGATCTTTTCTACGGGGTCTGACGC
6480
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BspHI

DraI

TCAGTGGAACGAAAACACGTTAAGGGATTTTGGTCATGAGATTATCAAAAAGGATCTTCACCTAGATCCTTTTAAATT
6560
AGTCACCTTGCTTTGAGTGCAATTCCTAAAACAGTACTCTAATAGTTTTTCTAGAAGTGGATCTAGGAAAATTTAA

DraI

AAAAATGAAGTTTTAAATCAATCTAAAGTATATATGAGTAACTTGGTCTGACAGTTACCAATGCTTAATCAGTGAGGCA
6640
TTTTTACTTCAAATTTAGTTAGATTTTCAATATATACTCATTTGAACCAGACTGTCAATGGTTACGAATTAGTCACTCCGT

• Trp His Lys Ile Leu Ser Ala
AMP

CCTATCTCAGCGATCTGTCTATTTTCGTTTCATCCATAGTTGCCTGACTCCCCGTCGTGTAGATAACTACGATACGGGAGGG
6720
GGATAGAGTCGCTAGACAGATAAAGCAAGTAGGTATCAACGGACTGAGGGGCAGCACATCTATTGATGCTATGCCCTCCC
Gly Ile Glu Ala Ile Gln Arg Asn Arg Glu Asp Met Thr Ala Gln Ser Gly Thr Thr Tyr Ile Val Val Ile Arg Ser Pro
AMP

CTTACCATCTGGCCCCAGTGCTGCAATGATACCGCGAGACCCACGCTCACC GGCTCCAGATTTATCAGCAATAAACCAGC
6800
GAATGGTAGACCGGGGTCACGACGTTACTATGGCGCTCTGGGTGCGAGTGGCCGAGGTCTAAATAGTCGTTATTTGGTCC
Lys Gly Asp Pro Gly Leu Ala Ala Ile Ile Gly Arg Ser Gly Arg Glu Gly Ala Gly Ser Lys Asp Ala Ile Phe Trp Gly
AMP

CAGCCGGAAGGGCCGAGCGCAGAAGTGGTCCTGCAACTTTATCCGCCTCCATCCAGTCTATTAATTGTTGCCGGGAAGCT
6880
GTCGGCCTTCCCGGCTCGCGTCTTACCAGGACGTTGAAATAGGCGGAGGTAGGTACAGATAATTAACAACGGCCCTTCGA
Ala Pro Leu Ala Ser Arg Leu Leu Pro Gly Ala Val Lys Asp Ala Glu Met Trp Asp Ile Leu Gln Gln Arg Ser Ala
AMP

FspI

PstI

AGAGTAAGTAGTTCGCCAGTTAATAGTTTTCGCAACGTTGTTGCCATTGCTGCAGGCATCGTGGTGTACGCTCGTCGTT
6960
TCTCATTTCATCAAGCGGTCAATTATCAAACGCGTTGCAACAACGGTAACGACGTCCGTAGCACCACAGTGCGAGCAGCAA
Leu Thr Leu Leu Glu Gly Thr Leu Leu Lys Arg Leu Thr Thr Ala Met Ala Ala Pro Met Thr Thr Asp Arg Glu Asp Asn
AMP

TGGTATGGCTTCATTTCAGCTCCGGTTCCCAACGATCAAGGCGAGTTACATGATCCCCCATGTTGTGCAAAAAAGCGGTTA
7040
ACCATACCGAAGTAAGTCGAGGCCAAGGGTTGCTAGTTCCGCTCAATGTACTAGGGGGTACAACACGTTTTTTCGCCAAT
Pro Ile Ala Glu Asn Leu Glu Pro Glu Trp Arg Asp Leu Arg Thr Val His Asp Gly Met Asn His Leu Phe Ala Thr Leu
AMP

PvuI

GCTCCTTCGGTCCTCCGATCGTTGTCAGAAGTAAGTTGGCCGCAGTGTTATCACTCATGGTTATGGCAGCACTGCATAAT 7120
CGAGGAAGCCAGGAGGCTAGCAACAGTCTTCATTCAACCGGCGTCACAATAGTGAGTACCAATACCGTCGTGACGTATTA
Glu Lys Pro Gly Gly Ile Thr Thr Leu Leu Leu Asn Ala Ala Thr Asn Asp Ser Met Thr Ile Ala Ala Ser Cys Leu
AMP

TCTCTTACTGTCATGCCATCCGTAAGATGCTTTTCTGTGACTGGTGAGTACTCAACCAAGTCATTCTGAGAATAGTGTAT 7200
AGAGAATGACAGTACGGTAGGCATTCTACGAAAAGACACTGACCACTCATGAGTTGGTTCAGTAAGACTCTTATCACATA
Glu Arg Val Thr Met Gly Asp Thr Leu His Lys Glu Thr Val Pro Ser Tyr Glu Val Leu Asp Asn Gln Ser Tyr His Ile
AMP

DraI

GCGGCGACCGAGTTGCTCTTGCCCGGCGTCAACACGGGATAATACCGCGCCACATAGCAGAACTTTAAAGTGCTCATCA 7280
CGCCGCTGGCTCAACGAGAACGGGCGCAGTTGTGCCCTATTATGGCGCGGTGTATCGTCTTGAAATTTTCACGAGTAGT
Arg Arg Gly Leu Gln Glu Gln Gly Ala Asp Val Arg Ser Leu Val Ala Gly Cys Leu Leu Val Lys Phe Thr Ser Met Met
AMP

TTGGAACAGTTCTTCGGGGCGAAACTCTCAAGGATCTTACCGCTGTTGAGATCCAGTTCGATGTAACCCACTCGTGCA 7360
AACCTTTTGCAAGAAGCCCCGCTTTTGAGAGTTCCTAGAATGGCGACAACCTCTAGGTCAAGCTACATTGGGTGAGCACGT
Pro Phe Arg Glu Glu Pro Arg Phe Ser Glu Leu Ile Lys Gly Ser Asn Leu Asp Leu Glu Ile Tyr Gly Val Arg Ala
AMP

CCCACTGATCTTCAGCATCTTTTACTTTTACCAGCGTTTCTGGGTGAGCAAAAACAGGAAGGCAAAATGCCGCAAAAAA 7440
GGGTTGACTAGAAGTCGTAGAAAATGAAAGTGGTCGAAAGACCCACTCGTTTTTGTCTTCCGTTTACGGCGTTTTT
Gly Leu Gln Asp Glu Ala Asp Lys Val Lys Val Leu Thr Glu Pro His Ala Phe Val Pro Leu Cys Phe Ala Ala Phe Phe
AMP

GGGAATAAGGGCGACACGGAATGTTGAATACTCATACTCTTCTTTTTCAATATTATTGAAGCATTTATCAGGGTTATT 7520
CCCTTATTTCCGCTGTGCCTTTACAACCTATGAGTATGAGAAGGAAAAAGTTATAATAACTTCGTAAATAGTCCCAATAA
Pro Ile Leu Ala Val Arg Phe His Gln Ile Ser Met
AMP

BspHI

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CAGAGTACTCGCTATGTATAAATTACATAAATCTTTTTATTTGTTTATCCCAAGGCGCGTGTAAGGGGCTTTTCAC

BspHI

CCACCTGACGTCTAAGAAACCATTATTATCATGACATTAACCTATAAAAATAGGCGTATCACGAGGCCCTTTTCGTCTTCA 7680
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AGAAT
→ 7685
TCTTA

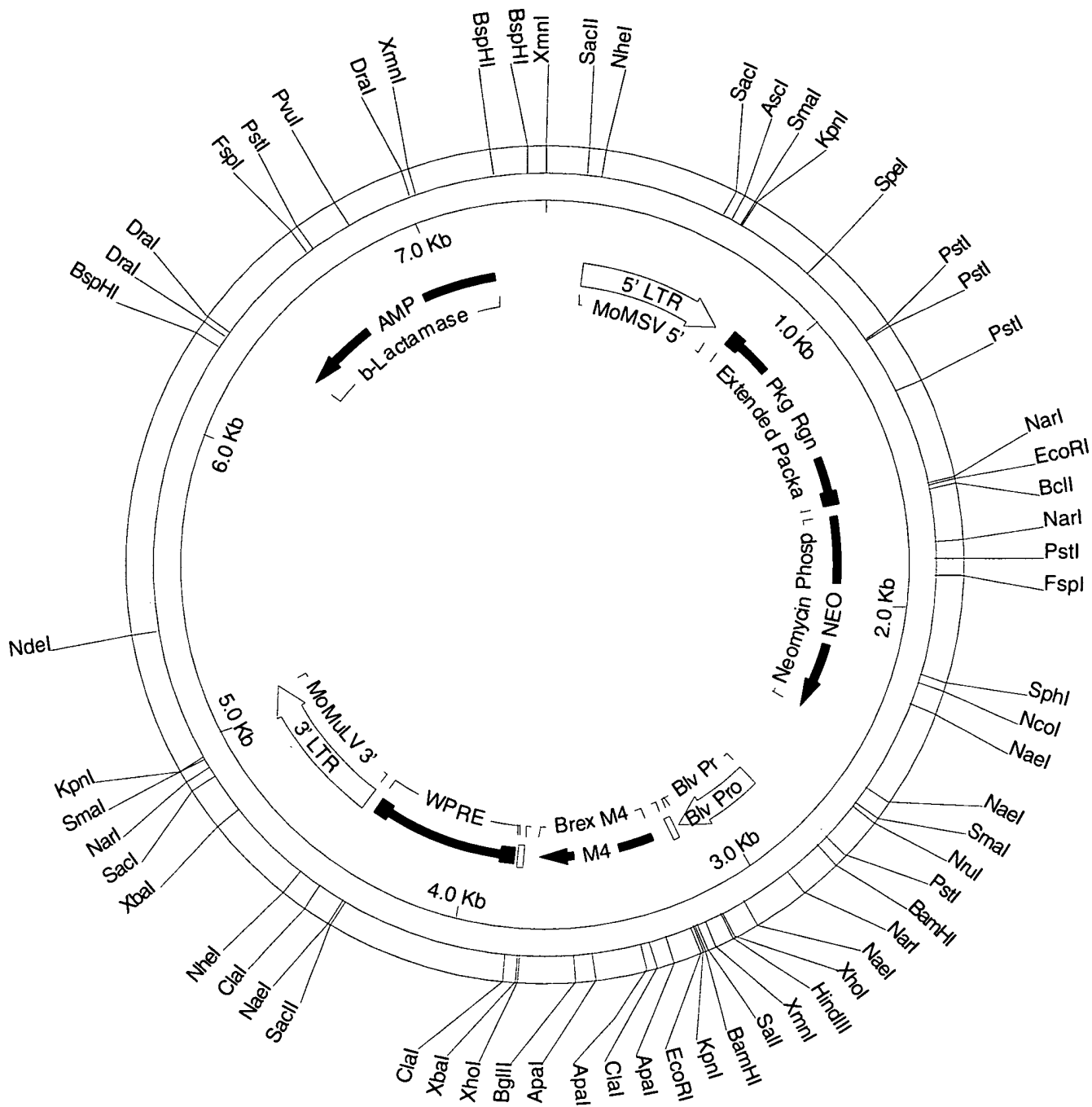


FIG. 11

FIG. 12

Page 1

Thursday, June 13, 2002 3:55 PM

GD2415 (pLNBlv-M4W).MPD (1 > 7428) Site and Sequence

Enzymes : 35 of 538 enzymes (Filtered)

Settings : Circular, Certain Sites Only, Standard Genetic Code

XmnI

GAATTAATTCATACCAGATCACCGAAAACGTGCTCTCAAATGTGTCCCCCTCACACTCCCAAATTCGCGGGCTTCTGCCT
CTTAATTAAGTATGGTCTAGTGGCTTTTGACAGGAGGTTTACACAGGGGGAGTGTGAGGGTTTAAGCGCCCAAGACGGA

SacII

CTTAGACCACTCTACCCTATTCCTCCACACTCACCGGAGCCAAAGCCGCGCCCTTCCGTTTCTTTGCTTTTGAAGACCC
GAATCTGGTGAGATGGGATAAGGGGTGTGAGTGGCTCGGTTTCGGCGCCGGGAAGGCAAAGAAACGAAAACCTTCTGGG

5' LTR

MoMSV 5' LTR

NheI

CACCCGTAGGTGGCAAGCTAGCTTAAGTAACGCCACTTTGCAAGGCATGGAAAAATACATAACTGAGAATAGAAAAGTTC
GTGGGCATCCACCGTTTCGATCGAATTCATTGCGGTGAAACGTTCCGTACCTTTTTATGTATTGACTCTTATCTTTTCAAG

5' LTR

MoMSV 5' LTR

AGATCAAGGTCAGGAACAAAGAAACAGCTGAATACCAAACAGGATATCTGTGGTAAGCGGTTCTTGCCCCGGCTCAGGGC
TCTAGTTCAGTCTTGTCTTTGTCGACTTATGGTTTGTCTATAGACACCATTCGCCAAGGACGGGGCCGAGTCCCG

5' LTR

MoMSV 5' LTR

CAAGAACAGATGAGACAGCTGAGTGATGGGCCAAACAGGATATCTGTGGTAAGCAGTTCCTGCCCCGGCTCGGGGCCAAG
GTTCTTGCTACTCTGTGACTCACTACCCGGTTTGTCTATAGACACCATTCGTCAAGGACGGGGCCGAGCCCCGGTTC

5' LTR

MoMSV 5' LTR

AACAGATGGTCCCCAGATGCGGTCCAGCCCTCAGCAGTTTCTAGTGAATCATCAGATGTTTCCAGGGTGCCCCAAGGACC
TTGTCTACCAGGGGTCTACGCCAGGTGCGGAGTCGTCAAAGATCACTTAGTAGTCTACAAAGGTCCCACGGGGTTCCTGG

5' LTR

MoMSV 5' LTR

TGAAAATGACCCTGTACCTTATTTGAACTAACCAATCAGTTCGCTTCTCGCTTCTGTTTCGCGCGCTTCCGCTCTCCGAGC
ACTTTTACTGGGACATGGAATAAACTTGATTGGTTAGTCAAGCGAAGAGCGAAGACAAGCGCGCGAAGGCGAGAGGCTCG

5' LTR

MoMSV 5' LTR

SacI

Ascl

SmaI

KpnI

TCAATAAAGAGCCCAACAACCCCTCACTCGGCGCGCCAGTCTTCCGATAGACTGCGTCGCCCGGGTACCCGTATTCCCAA
AGTTATTTTCTCGGGTGTGGGGAGTGAGCCGCGCGGTGAGAAGGCTATCTGACGCAGCGGGCCCATGGGCATAAGGGTT

5' LTR

MoMSV 5' LTR

TAAAGCCTCTTGCTGTTTGCATCCGAATCGTGGTCTCGCTGTTCTTGGGAGGGTCTCCTCTGAGTGATTGACTACCCAC 720
 ATTCGGAGAACGACAAACGTAGGCTTAGCACCAGAGCGACAAGGAACCTCCCAGAGGAGACTCACTAACTGATGGGTG
 5' LTR
 MoMSV 5' LTR

GACGGGGTCTTTTCATTTGGGGGCTCGTCCGGGATTTGGAGACCCCTGCCAGGGACCACCGACCCACCACCGGGAGGTA 800
 CTGCCCCCAGAAAGTAAACCCCCGAGCAGGCCCTAAACCTCTGGGGACGGTCCCTGGTGGCTGGGTGGTGGCCCTCCAT
 5' LTR
 MoMSV 5' LTR

AGCTGGCCAGCAACTTATCTGTGTCTGTCCGATTGTCTAGTGTCTATGTTTGATGTTATGCGCTGCGTCTGTACTAGTT 880
 TCGACCGGTGCTTGAATAGACACAGACAGGCTAACAGATCACAGATACAACTACAATACGGGACGCAGACATGATCAA
 Pkg Rgn
 Extended Packaging Region

AGCTAACTAGCTCTGTATCTGGCGGACCCGTGGTGGAACTGACGAGTTCTGAACACCCGGCCGCAACCCTGGGAGACGTC 960
 TCGATTGATCGAGACATAGACCGCTGGGCACCACCTTGACTGTCAAGACTTGTGGGCCGGCGTTGGGACCCCTCTGCAG
 Pkg Rgn
 Extended Packaging Region

CCAGGGACTTTGGGGGCCGTTTTTGTGGCCCGACCTGAGGAAGGGAGTCGATGTGGAATCCGACCCCGTCAGGATATGTG 1040
 GGTCCCTGAAACCCCGGCAAAAACACCGGGCTGGACTCCTTCCCTCAGCTACACCTTAGGCTGGGGCAGTCTTATACAC
 Pkg Rgn
 Extended Packaging Region

GTTCTGGTAGGAGACGAGAACCTAAACAGTTCCCGCCTCCGTCTGAATTTTTGCTTTTCGGTTTGGAAACGAAGCCGCGC 1120
 CAAGACCATCCTCTGCTCTTGGATTTGTCAAGGGCGGAGGCAGACTTAAAAACGAAAGCCAAACCTTGGCTTCGGCGCG
 Pkg Rgn
 Extended Packaging Region

PstI PstI
 GTCTTGCTGCTGCAGCGCTGCAGCATCGTTCTGTGTTGTCTCTGTCTGACTGTGTTTCTGTATTTGTCTGAAAATTAGG 1200
 CAGAACAGACGACGTCGCGACGTCGTAGCAAGACACAACAGAGACAGACTGACACAAAGACATAAACAGACTTTTAATCC
 Pkg Rgn
 Extended Packaging Region

GCCAGACTGTTACCACTCCCTTAAGTTTGACCTTAGGTCACTGGAAAGATGTCGAGCGGATCGCTCACAACCAGTCGGTA 1280
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 Pkg Rgn
 Extended Packaging Region

PstI

GATGTCAAGAAGAGACGTTGGGTACCTTCTGCTCTGCAGAATGGCCAACCTTTAACGTCGGATGGCCGCGAGACGGCAC
CTACAGTTCTTCTCTGCAACCCAATGGAAGACGAGACGCTCTTACCGGTTGGAAATTGCAGCCTACCGGCGCTCTGCCGTG 1360

- Pkg Rgn

- Extended Packaging Region

CTTTAACCGAGACCTCATCACCCAGGTTAAGATCAAGGTCTTTTACCTGGCCCGCATGGACACCCAGACCAGGTCCCTT
GAAATTGGCTCTGGAGTAGTGGGTCCAATTCTAGTTCAGAAAAGTGGACCGGGCGTACCTGTGGGTCTGGTCCAGGGGA 1440

- Pkg Rgn

- Extended Packaging Region

ACATCGTGACCTGGGAAGCCTTGGCTTTTGACCCCCCTCCCTGGGTCAAGCCCTTTGTACACCCTAAGCCTCCGCCTCCT
TGTAGCACTGGACCCTTCGGAACCGAAAACCTGGGGGAGGGACCCAGTTTCGGGAAACATGTGGGATTCGGAGGCGGAGGA 1520

- Pkg Rgn

- Extended Packaging Region

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1600
GAAGGAGGTAGGCGGGGCAGAGAGGGGGAAC TTGGAGGAGCAAGCTGGGGCGGAGCTAGGAGGGAAATAGGTCGGGAGTG

- Pkg Rgn

- Extended Packaging Region

Narl

EcoRI

BcII

TCCTTCTCTAGGCGCCGAATTCCGATCTGATCAAGAGACAGGATGAGGATCGTTTCGCATGATTGAACAAGATGGATTG
AGGAAGAGATCCGCGGCCTTAAGGCTAGACTAGTTCTCTGTCTACTCCTAGCAAAGCGTACTAACTTGTCTACCTAAC 1680

— Pkg Rgn —
- Extended Packaging-

Met Ile Glu Gln Asp Gly Leu
Neomycin Phosphotransfer-

CACGCAGGTTCTCCGGCCGCTTGGGTGGAGAGGCTATTGGCTATGACTGGGCACAACAGACAATCGGCTGCTCTGATGC
GTGCGTCCAAGAGGCCGGCGAAGCCACCTCTCCGATAAGCCGATACTGACCCGTGTTGTCTGTTAGCCGACGAGACTACG 1760

His Ala Gly Ser Pro Ala Ala Trp Val Glu Arg Leu Phe Gly Tyr Asp Trp Ala Gln Gln Thr Ile Gly Cys Ser Asp Ala
Neomycin Phosphotransferase

Narl

CGCCGTGTTCCGGCTGTCAGCGCAGGGGCGCCGGTCTTTTTGTCAAGACCGACCTGTCCGGTGCCCTGAATGAAGTGC 1840
GCGGCACAAGGCCGACAGTTCGCGTCCCCGCGGGCCAAGAAAAACAGTTCTGGCTGGACAGGCCACGGGACTTACTTGACG

Ala Val Phe Arg Leu Ser Ala Gln Gly Arg Pro Val Leu Phe Val Lys Thr Asp Leu Ser Gly Ala Leu Asn Glu Leu

- Neomycin Phosphotransferase

PstI

Fspl

AGGACGAGGCAGCGCGGCTATCGTGGCTGGCCACGACGGGCGTTTCCTTGCGCAGCTGTGCTCGACGTTGCTACTGAAGCG
 TCCTGCTCCGTCGCGCCGATAGCACCGACCGGTGCTGCCCGCAAGGAACGCGTGCACACGAGCTGCAACAGTGACTTCGC

Gln Asp Glu Ala Ala Arg Leu Ser Trp Leu Ala Thr Thr Gly Val Pro Cys Ala Ala Val Leu Asp Val Val Thr Glu Ala

- Neomycin Phosphotransferase

GGAAGGGACTGGCTGCTATTGGGCGAAGTGCCGGGGCAGGATCTCCTGTATCTCACCTTGCTCCTGCCGAGAAAGTATC
 CCTTCCCTGACCGACGATAACCCGCTTCACGGCCCCGTCCTAGAGGACAGTAGAGTGGAACGAGGACGGCTCTTTTCATAG
 Gly Arg Asp Trp Leu Leu Leu Gly Glu Val Pro Gly Gln Asp Leu Leu Ser Ser His Leu Ala Pro Ala Glu Lys Val Ser
Neomycin Phosphotransferase

CATCATGGCTGATGCAATGCGGCGGCTGCATACGCTTGATCCGGCTACCTGCCCATTCGACCACCAAGCGAAACATCGCA
 GTAGTACCGACTACGTTACGCCGCCGACGATATGCGAACTAGGCCGATGGACGGGTAAAGCTGGTGGTTCGCTTTGTAGCGT

Ile Met Ala Asp Ala Met Arg Arg Leu His Thr Leu Asp Pro Ala Thr Cys Pro Phe Asp His Gln Ala Lys His Arg

Neomycin Phosphotransferase

TCGAGCGAGCACGTACTCGGAITGGAAGCCGGTCTTGTCGATCAGGATGATCTGGACGAAGAGCATCAGGGGCTCGCGCCA
AGCTCGCTCGTGATGAGCCTACCTTCGGCCAGAACAGCTAGTCCTACTAGACCTGCTTCTCGTAGTCCCCGAGCGCGGT
Ile Glu Arg Ala Arg Thr Arg Met Glu Ala Gly Leu Val Asp Gln Asp Asp Leu Asp Glu Glu His Gln Gly Leu Ala Pro
Neomycin Phosphotransferase

GAATATCATGGTGGAAATGGCCGCTTTTCTGGATTCATCGACTGTGGCCGGCTGGGTGTGGCGGACCGCTATCAGGACA
 CTTATAGTACCACCTTTTACGGCGAAAAGACCTAAGTAGCTGACACCGGCCGACCCACACCGCTGGCGATAGTCTCTGT
 Asn Ile Met Val Glu Asn Gly Arg Phe Ser Gly Phe Ile Asp Cys Gly Arg Leu Gly Val Ala Asp Arg Tyr Gln Asp
 Neomycin Phosphotransferase

TAGCGTTGGCTACCCGTGATATTGCTGAAGAGCTTGGCGGCGAATGGGCTGACCGCTTCTCGTGCTTTACGGTATCGCC
 ATCGCAACCGATGGGCACTATAACGACTTCTCGAACCGCCGCTTACCCGACTGGCGAAGGAGCACGAAATGCCATAGCGG

Ile Ala Leu Ala Thr Arg Asp Ile Ala Glu Glu Leu Gly Gly Glu Trp Ala Asp Arg Phe Leu Val Leu Tyr Gly Ile Ala

Neomycin Phosphotransferase

GCTCCCGATTGCGAGCGCATCGCCTTCTATCGCCTTCTTGACGAGTTCTTCTGAGCGGGACTCTGGGGTTTCGAAATGACC 2480
 CGAGGGCTAAGCGTCGCGTAGCGGAAGATAGCGGAAGAACTGCTCAAGAAGACTCGCCCTGAGACCCCAAGCTTTACTGG
 Ala Pro Asp Ser Gln Arg Ile Ala Phe Tyr Arg Leu Leu Asp Glu Phe Phe •
 Neomycin Phosphotransferase

GACCAAGCGACGCCAACCTGCCATCACGAGATTTGATTCCACGCGCGCTTCTATGAAAGGTTGGGCTTCGGAATCGT 2560
CTGGTTCGCTGCGGGTTGGACGGTAGTGCTCTAAAGCTAAGGTGGCGGCGGAAGATACTTTCCAACCCGAAGCCTTAGCA

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NruI

TCGCGAGTTGGTTCAGCTGCTGCCTGAGGCTGGACGACCTCGCGGAGTTCTACCGGCAGTGCAAATCCGTCGGCATCCAG
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PstI

GAAACCAGCAGCGGCTATCCGCGCATCCATGCCCCGAAGTGCAGGAGTGGGGAGGCACGATGGCCGCTTTGGTCGAGGC
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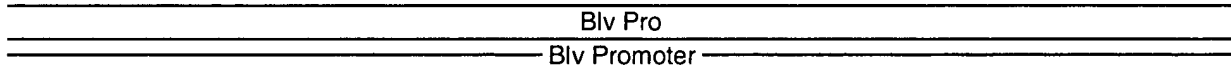
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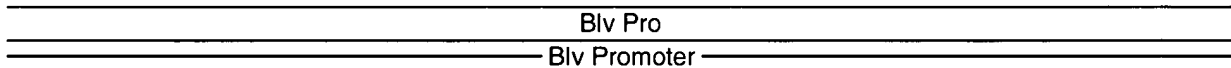


NarI

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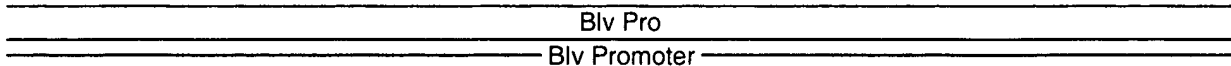


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NaeI

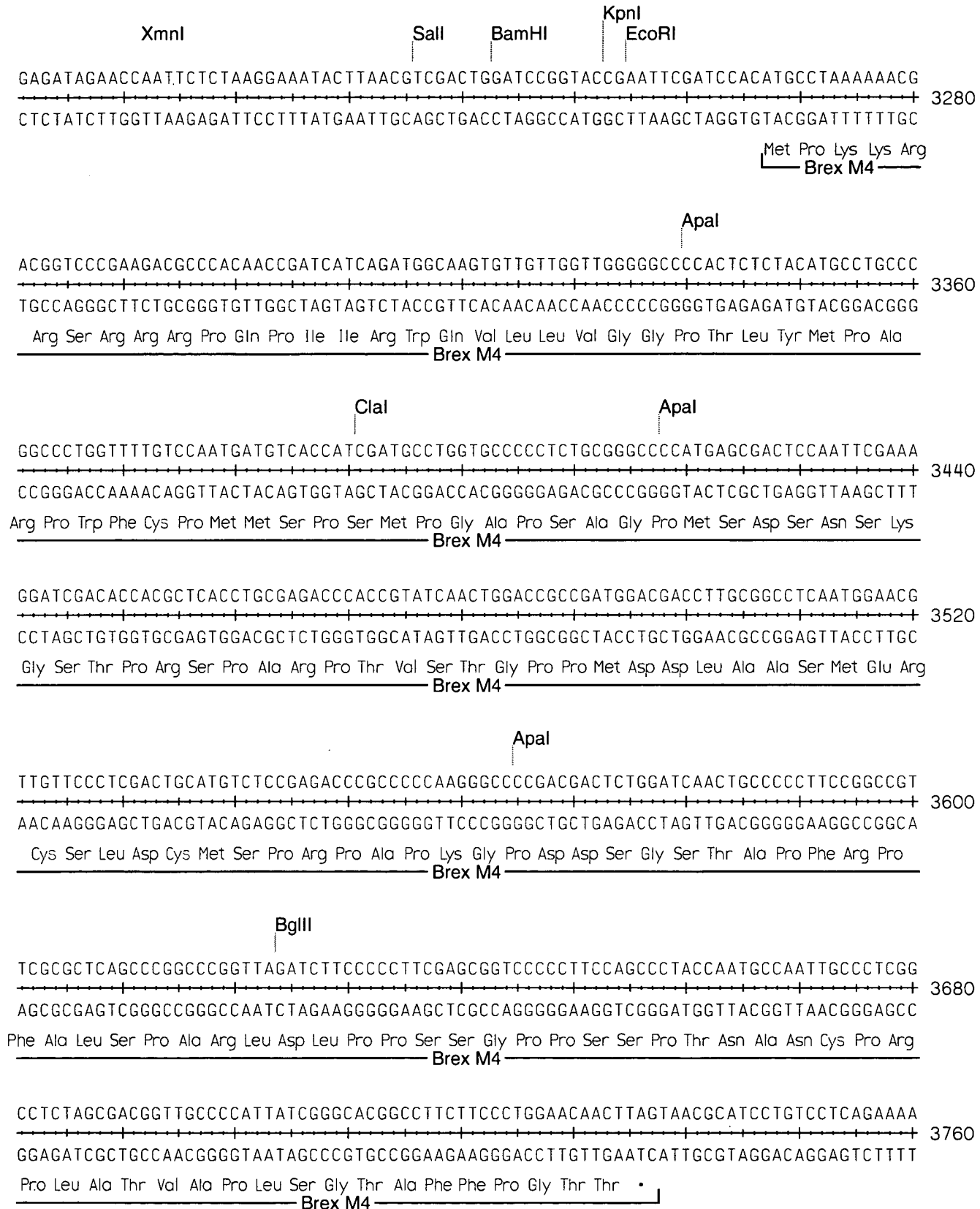
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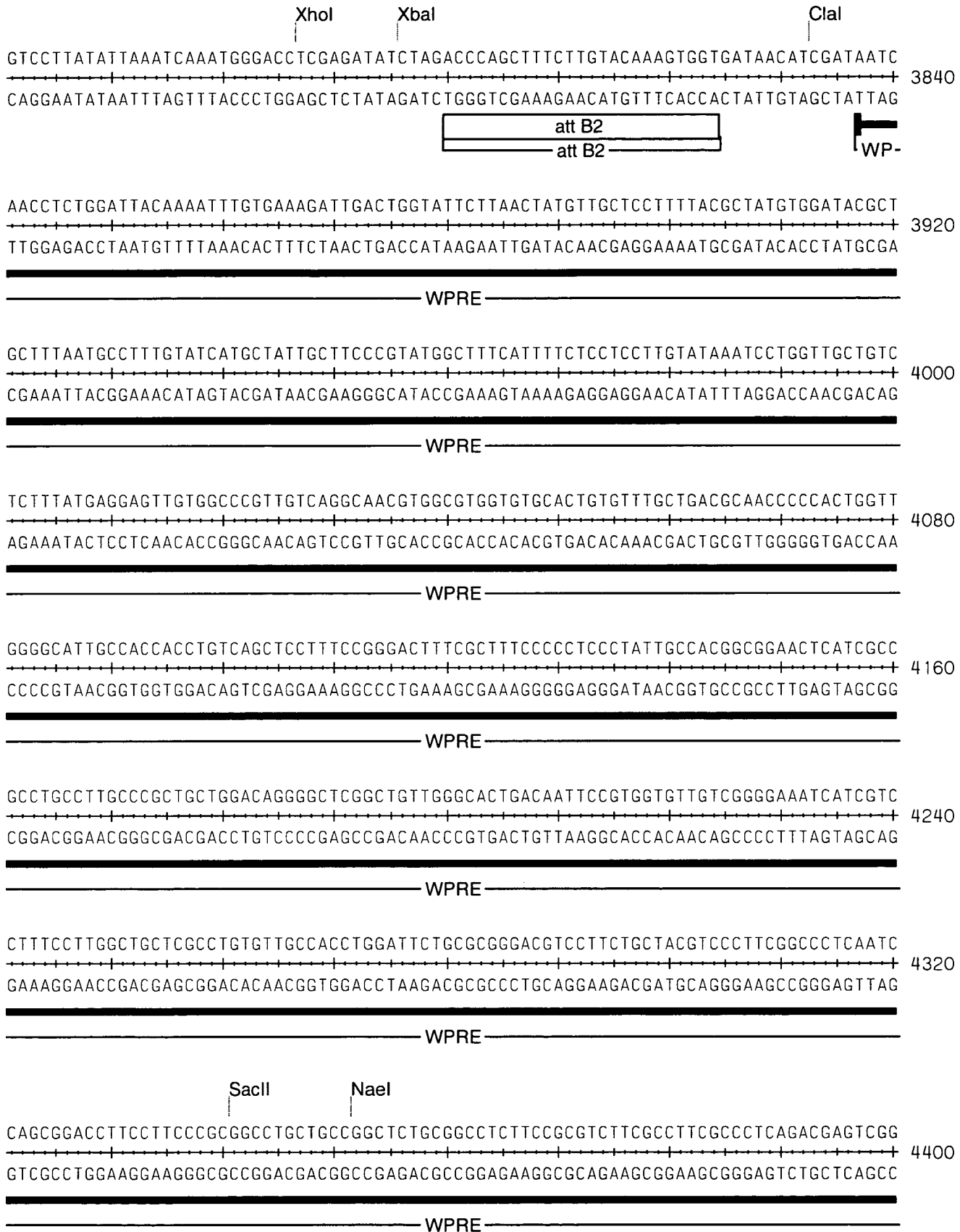
XhoI HindIII

TGAGACCCTCGTGCTCAGCTCTCGGTCCTGCCTCGAGAAGCTTGTATCACAAGTTTGTACAAAAAGCAGGCTTCGAAG
ACTCTGGGAGCAGAGTCGAGAGCCAGGACGGAGCTCTTCGAACAATAGTGTTCAAACATGTTTTTCGTCCGAAGCTTC 3200





Thursday, June 13, 2002 3:55 PM
GD2415 (pLNBlv-M4W).MPD (1 > 7428) Site and Sequence



Thursday, June 13, 2002 3:55 PM
GD2415 (pLNBlv-M4W).MPD (1 > 7428) Site and Sequence

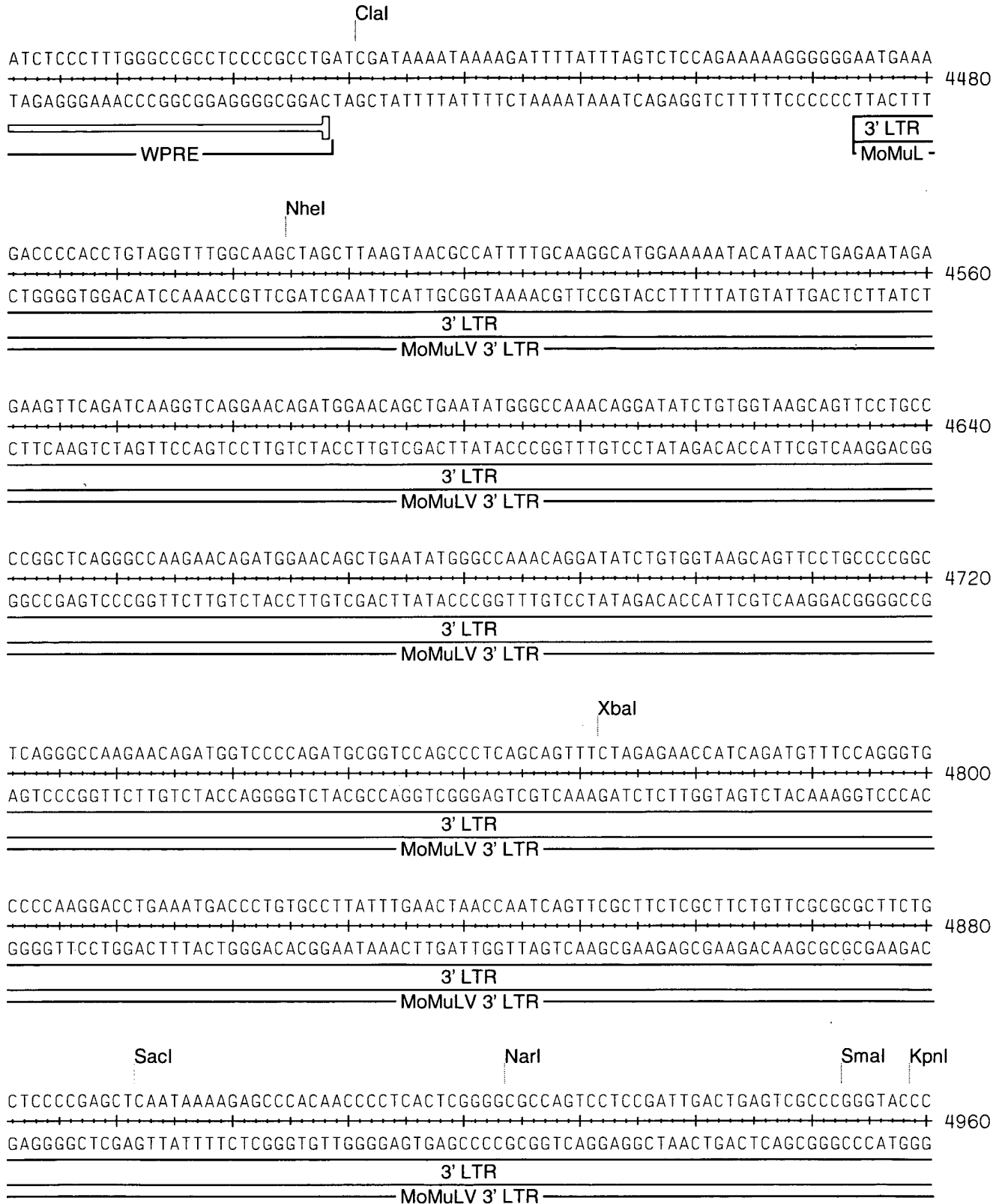


FIG. 12 (cont)

Thursday, June 13, 2002 3:55 PM

GD2415 (pLNBiv-M4W).MPD (1 > 7428) Site and Sequence

Page 9

GTGTATCCAATAAACCCCTCTTGCAGTTGCATCCGACTTGTGGTCTCGCTGTTCCCTTGGGAGGGTCTCCTCTGAGTGATTG 5040
CACATAGGTTATTTGGGAGAACGTCAACGTAGGCTGAACACCAGAGCGACAAGGAACCCCTCCCAGAGGAGACTCACTAAC
3' LTR
MoMuLV 3' LTR

ACTACCGTCAGCGGGGTCTTTCATTTGGGGGCTCGTCCGGGATCGGGAGACCCCTGCCAGGGACCACCGACCCACCA 5120
TGATGGGCAGTCGCCCCAGAAAAGTAAACCCCCGAGCAGGCCCTAGCCCTCTGGGGACGGGTCCCTGGTGGCTGGGTGGT
3' LTR
MoMuLV 3' LTR

CCGGGAGGTAAGCTGGCTGCCTCGCGGTTTTCGGTGATGACGGTGAAAACCTCTGACACATGCAGCTCCCGGAGACGGTC 5200
GGCCCTCCATTGACCGACGGAGCGCGCAAAGCCACTACTGCCACTTTTGGAGACTGTGTACGTCGAGGGCCTCTGCCAG

ACAGCTTGTCTGTAAGCGGATGCCGGGAGCAGACAAGCCCGTCAGGGCGGTCAGCGGGTGTGGCGGGTGTGGGGGCGC 5280
TGTCGAACAGACATTGCCTACGGCCCTCGTCTGTTTCGGGCAGTCCCGCGCAGTCGCCACAACCGCCACAGCCCCGCG

AGCCATGACCCAGTCACGTAGCGATAGCGGAGTGTATACTGGCTTAACTATGCGGCATCAGAGCAGATTGTAAGTACTGAGAGT 5360
TCGGTACTGGGTCAGTGCATCGCTATCGCCTCACATATGACCGAATTGATACGCCGTAGTCTCGTCTAACATGACTCTCA

NdeI

GCACCATATGCGGTGTGAAATACCGCACAGATGCGTAAGGAGAAAATACCGCATCAGGCGCTCTTCCGCTTCTCGCTCA 5440
CGTGGTATACGCCACACTTTATGGCGTGTCTACGCATTCTCTTTATGGCGTAGTCCGCGAGAAGGCGAAGGAGCGAGT

CTGACTCGCTGCGCTCGGTCTGTTTCGGCTGCGGCGAGCGGTATCAGCTCACTCAAAGGCGGTAATACGGTTATCCACAGAA 5520
GACTGAGCGACGCGAGCCAGCAAGCCGACGCCGCTCGCCATAGTCGAGTGAGTTTCCGCCATTATGCCAATAGGTGTCTT

TCAGGGGATAACGCAGGAAAGAACATGTGAGCAAAAGGCCAGCAAAAGGCCAGGAACCGTAAAAAGGCCGCTTGCTGGC 5600
AGTCCCCTATTGCGTCTTTCTTGTACACTCGTTTTCCGGTCGTTTTCCGGTCCTTGGCATTTTTCCGGCGCAACGACCG

GTTTTTCCATAGGCTCCGCCCCCTGACGAGCATCACAAAAATCGACGCTCAAGTCAGAGGTGGCGAAACCCGACAGGAC 5680
CAAAAAGGTATCCGAGGCGGGGGGACTGCTCGTAGTGTTTTAGCTGCGAGTTCAGTCTCCACCGCTTTGGGCTGTCTTG

TATAAAGATACCAGGCGTTTTCCCTGGAAGCTCCCTCGTGGCTCTCCTGTTCCGACCTGCCGCTTACCGGATACCTG 5760
ATATTTCTATGGTCCGCAAAGGGGGACCTTCGAGGGAGCACGCGAGAGGACAAGGCTGGGACGGCGAATGGCCTATGGAC

TCCGCTTTCTCCCTTCGGGAAGCGTGGCGCTTTCTCATAGCTCACGCTGTAGGTATCTCAGTTCGGTGTAGGTCGTTTCG 5840
AGGCGGAAAGAGGGAAGCCCTTCGCACCGCGAAAGAGTATCGAGTGCGACATCCATAGAGTCAAGCCACATCCAGCAAGC

CTCCAAGCTGGGCTGTGTGCACGAACCCCCGTTTCAGCCCGACCGTGCCTTATCCGGTAACTATCGTCTTGAGTCCA 5920
GAGGTTTCGACCCGACACACGTGCTTGGGGGGCAAGTCGGCTGGCGACGCGGAATAGGCCATTGATAGCAGAACTCAGGT

Thursday, June 13, 2002 3:55 PM

GD2415 (pLNBlv-M4W).MPD (1 > 7428) Site and Sequence

ACCCGGTAAGACACGACTTATCGCCACTGGCAGCAGCCACTGGTAACAGGATTAGCAGAGCGAGGTATGTAGGCGGTGCT
TGGGCCATTCTGTGCTGAATAGCGGTGACCGTCGTCGGTGACCATTTGCTTAATCGTCTCGCTCCATACATCCGCCACGA

6000

ACAGAGTTCTTGAAGTGGTGGCCTAACTACGGCTACACTAGAAGGACAGTATTTGGTATCTGCGCTCTGCTGAAGCCAGT
TGTCTCAAGAACTTCACCACCGGATTGATGCCGATGTGATCTTCTGTCATAAACCATAGACGCGAGACGACTTCGGTCA

6080

TACCTTCGGAAAAAGAGTTGGTAGCTCTTGATCCGGCAAACAAACCACCGCTGGTAGCGGTGGTTTTTTTGTITGCAAGC
ATGGAAGCCTTTTTCTCAACCATCGAGAACTAGGCCGTTTGTITGGTGGCGACCATCGCCACCAAAAAACAAACGTTTCG

6160

AGCAGATTACGCGCAGAAAAAAGGATCTCAAGAAGATCCTTTGATCTTTTCTACGGGGTCTGACGCTCAGTGAACGAA
TCGTCTAATGCGCGTCTTTTTTCTAGAGTTCTTCTAGGAACTAGAAAAGATGCCCCAGACTGCGAGTCACCTTGCTT

6240

BspHI

DraI

AACTCACGTAAAGGGATTTTGGTCATGAGATTATCAAAAAGGATCTTCACCTAGATCCTTTTAAATTAAAAATGAAGTTT
TTGAGTGCAATTCCTTAAAACAGTACTCTAATAGTTTTCTAGAAAGTGGATCTAGGAAAATTTAATTTTACTTCAAA

6320

DraI

TAAATCAATCTAAAGTATATATGAGTAAACTTGGTCTGACAGTTACCAATGCTTAATCAGTGAGGCACCTATCTCAGCGA
ATTTAGTTAGATTTTCATATATACTCATTGAACCAGACTGTCAATGGTTACGAATTAGTCACTCCGTGGATAGAGTCGCT

6400

• Trp His Lys Ile Leu Ser Ala Gly Ile Glu Ala Ile
b-Lactamase

TCTGTCTATTTCTGTTTCATCCATAGTTGCCTGACTCCCCGTCTGTGTAGATAACTACGATACGGGAGGGCTTACCATCTGGC
AGACAGATAAAGCAAGTAGGTATCAACGGACTGAGGGGCAGCACATCTATTGATGCTATGCCCTCCGAATGGTAGACCG

6480

Gln Arg Asn Arg Glu Asp Met Thr Ala Gln Ser Gly Thr Thr Tyr Ile Val Val Ile Arg Ser Pro Lys Gly Asp Pro
b-Lactamase

CCCAGTGCTGCAATGATACCGCGAGACCCACGCTCACC GGCTCCAGATTTATCAGCAATAAACCAGCCAGCCGGAAGGGC
GGGTACGACGTTACTATGGCGCTCTGGGTGCGAGTGCCGAGGTCTAAATAGTCGTTATTTGGTCGGTCGGCCTTCCCG

6560

Gly Leu Ala Ala Ile Ile Gly Arg Ser Gly Arg Glu Gly Ala Gly Ser Lys Asp Ala Ile Phe Trp Gly Ala Pro Leu Ala
b-Lactamase

CGAGCGCAGAAGTGGTCCTGCAACTTTATCCGCCTCCATCCAGTCTATTAATTGTTGCCGGAAGCTAGAGTAAGTAGTT
GCTCGCGTCTTACCAGGACGTTGAAATAGGCGGAGGTAGGTCAGATAATTAACAACGGCCCTTCGATCTCATTATCAA

6640

Ser Arg Leu Leu Pro Gly Ala Val Lys Asp Ala Glu Met Trp Asp Ile Leu Gln Gln Arg Ser Ala Leu Thr Leu Leu Glu
b-Lactamase

FspI

PstI

CGCCAGTTAATAGTTTGC GCAACGTTGTTGCCATTGCTGCAGGCATCGTGGTGTACGCTCGTCGTTTGGTATGGCTTCA
GCGGTCAATTATCAAACGCGTTGCAACAACGGTAACGACGTCCGTAGCACCACAGTGCGAGCAGCAAACCATACCGAAGT

6720

Gly Thr Leu Leu Lys Arg Leu Thr Thr Ala Met Ala Ala Pro Met Thr Thr Asp Arg Glu Asp Asn Pro Ile Ala Glu
b-Lactamase

Thursday, June 13, 2002 3:55 PM

GD2415 (pLNBiv-M4W).MPD (1 > 7428) Site and Sequence

TTCAGCTCCGGTTCCCAACGATCAAGGCGAGTTACATGATCCCCATGTTGTGCAAAAAGCGGTTAGCTCCTTCGGTCC 6800
 AAGTCGAGGCCAAGGGTTGCTAGTTCCGCTCAATGTACTAGGGGTACAACACGTTTTTTCGCCAATCGAGGAAGCCAGG
 Asn Leu Glu Pro Glu Trp Arg Asp Leu Arg Thr Val His Asp Gly Met Asn His Leu Phe Ala Thr Leu Glu Lys Pro Gly
 b-Lactamase

PvuI

TCCGATCGTTGTCAGAAGTAAGTTGGCCGCAGTGTATCACTCATGGTTATGGCAGCACTGCATAATTCTCTTACTGTCA 6880
 AGGCTAGCAACAGTCTTCAATTCAACCGGCGTCACAATAGTGAGTACCAATACCGTCGTGACGTATTAAGAGAATGACAGT
 Gly Ile Thr Thr Leu Leu Leu Asn Ala Ala Thr Asn Asp Ser Met Thr Ile Ala Ala Ser Cys Leu Glu Arg Val Thr Met
 b-Lactamase

TGCCATCCGTAAGATGCTTTTCTGTGACTGGTGAGTACTCAACCAAGTCATTCTGAGAATAGTGATGCGGCGACCGAGT 6960
 ACGGTAGGCATTCTACGAAAAGACACTGACCACTCATGAGTTGGTTCAGTAAGACTCTTATCACATACGCCGCTGGCTCA
 Gly Asp Thr Leu His Lys Glu Thr Val Pro Ser Tyr Glu Val Leu Asp Asn Gln Ser Tyr His Ile Arg Arg Gly Leu
 b-Lactamase

DraI

XmnI

TGCTCTTGCCCGGCGTCAACACGGGATAATACCGCGCCACATAGCAGAACTTTAAAAGTGCTCATCATTGGAAAACGTTT 7040
 ACGAGAACGGGCGCAGTTGTGCCCTATTATGGCGCGGTGTATCGTCTTGAAATTTTACGAGTAGTAACCTTTTGCAAG
 Gln Glu Gln Gly Ala Asp Val Arg Ser Leu Val Ala Gly Cys Leu Leu Val Lys Phe Thr Ser Met Met Pro Phe Arg Glu
 b-Lactamase

TTCGGGGCGAAAACCTCTCAAGGATCTTACCGCTGTTGAGATCCAGTTCGATGTAACCCACTCGTGACCCAACTGATCTT 7120
 AAGCCCCGCTTTTGAGAGTTCCCTAGAATGGCGACAACCTCTAGGTCAAGCTACATTGGGTGAGCACGTGGGTTGACTAGAA
 Glu Pro Arg Phe Ser Glu Leu Ile Lys Gly Ser Asn Leu Asp Leu Glu Ile Tyr Gly Val Arg Ala Gly Leu Gln Asp Glu
 b-Lactamase

CAGCATCTTTTACTTTACCCAGCGTTTCTGGGTGAGCAAAAACAGGAAGGCAAAATGCCGCAAAAAGGGAATAAGGGCG 7200
 GTCGTAGAAAATGAAAGTGGTCGAAAGACCACTCGTTTTTGTCTTCCGTTTTACGGCGTTTTTCCCTTATTCCCGC
 Ala Asp Lys Val Lys Val Leu Thr Glu Pro His Ala Phe Val Pro Leu Cys Phe Ala Ala Phe Phe Pro Ile Leu Ala
 b-Lactamase

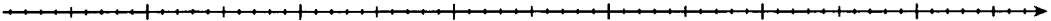
BspHI

ACACGGAAATGTTGAATACTCATACTCTTCCTTTTTCAATATTATTGAAGCATTTATCAGGGTTATTGTCTCATGAGCGG 7280
 TGTGCCCTTACAACCTTATGAGTATGAGAAGGAAAAAGTTATAATAACTTCGTAAATAGTCCCAATAACAGAGTACTCGCC
 Val Arg Phe His Gln Ile Ser Met
 b-Lactamase

ATACATATTTGAATGTATTTAGAAAAATAACAAATAGGGGTTCCGCGCACATTTCCCGAAAAGTGCCACCTGACGTCT 7360
 TATGTATAAACTTACATAAATCTTTTTATTTGTTTATCCCAAGGCGCGTGTAAAGGGGCTTTTCACGGTGGACTGCAGA

BspHI

AAGAAACCATTATTATCATGACATTAACTATAAAAAATAGGCGTATCACGAGGCCCTTTCGTCTTCAA
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7428

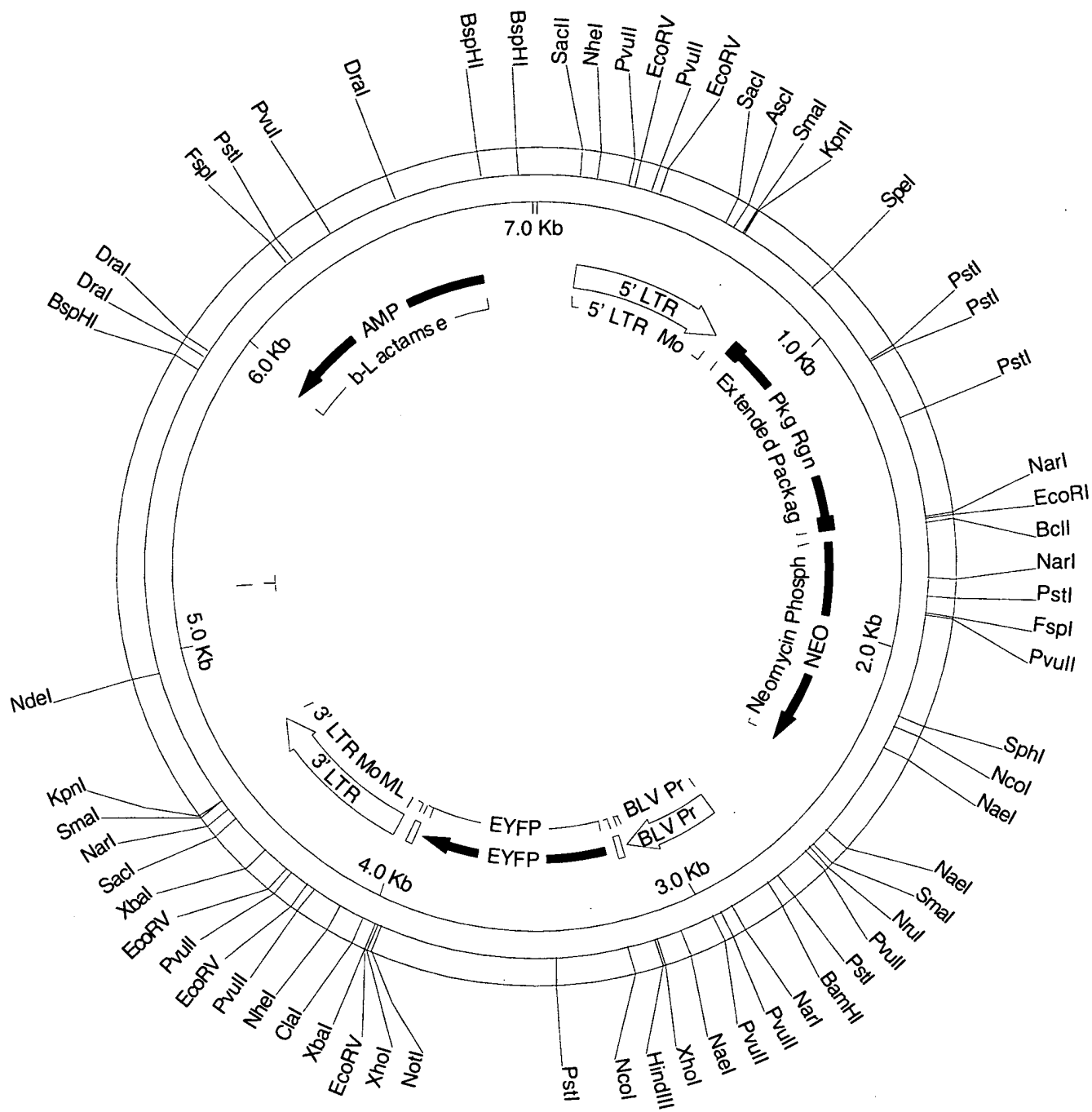


FIG. 13

FIG. 14

Thursday, June 13, 2002 3:42 PM

Page 1

GD2407 pLNBLV-YFP Map.MPD (1 > 7010) Site and Sequence

Enzymes : 36 of 538 enzymes (Filtered)

Settings : Circular, Certain Sites Only, Standard Genetic Code

GAATTAATTCATACCAGATCACCGAAAACTGTCTCCAAATGTGTCCCTCACACTCCCAAATTCGCGGGCTTCTGCCT
CTTAATTAAGTATGGTCTAGTGGCTTTTGACAGGAGGTTTACACAGGGGAGTGTGAGGGTTTAAGCGCCCGAAGACGGA

SacII

CTTAGACCACTCTACCCTATTCCTCCACACTCACCGGAGCCAAAGCCGCGGCCCTTCCGTTTCTTTGCTTTTGAAAGACCC
GAATCTGGTGAGATGGGATAAGGGGTGTGAGTGGCTTCGGTTTCGGCGCCGGGAAGGCAAAGAAACGAAAACTTTCTGGG

5' LTR

5' LTR MoMS-

NheI

CACCCGTAGGTGGCAAGCTAGCTTAAGTAACGCCACTTTGCAAGGCATGGAAAAATACATAACTGAGAATAGAAAAGTTC
GTGGGCATCCACCGTTCGATCGAATTCATTGCGGTGAAACGTTCCGTACCTTTTATGTATTGACTCTTATCTTTTCAAG

5' LTR

5' LTR MoMSV

PvuII

EcoRV

AGATCAAGGTCAGGAACAAAGAAACAGCTGAATACCAAACAGGATATCTGTGGTAAGCGGTTCTTGCCCCGGCTCAGGGC
TCTAGTTCCAGTCCTTGTTTCTTTGTGCACTTATGGTTTGTCTATAGACACCATTCGCCAAGGACGGGGCCGAGTCCCG

5' LTR

5' LTR MoMSV

PvuII

EcoRV

CAAGAACAGATGAGACAGCTGAGTGATGGGCCAAACAGGATATCTGTGGTAAGCAGTTCTTGCCCCGGCTCGGGGCCAAG
GTTCTTGTCTACTCTGTGCACTCACTACCCGGTTTGTCTATAGACACCATTCGTC AAGGACGGGGCCGAGCCCCGGTTC

5' LTR

5' LTR MoMSV

AACAGATGGTCCCCAGATGCGGTCCAGCCCTCAGCAGTTTCTAGTGAATCATCAGATGTTTCCAGGGTGCCCCAAGGACC
TTGTCTACCAGGGGTCTACGCCAGGTCGGGAGTCGTCAAAGATCACTTAGTAGTCTACAAAGGTCCACGGGGTTCTCTGG

5' LTR

5' LTR MoMSV

TGAAAATGACCCTGTACCTTATTTGAACTAACCAATCAGTTCGCTTCTCGCTTCTGTTTCGCGCGCTTCCGCTCTCCGAGC
ACTTTTACTGGGACATGGAATAAACTTGATTGGTTAGTCAAGCGAAGAGCGAAGACAAGCGCGCGAAGGCGAGAGGCTCG

5' LTR

5' LTR MoMSV

FIG. 14 (cont)

Thursday, June 13, 2002 3:42 PM

Page 2

GD2407 pNLBV-YFP Map.MPD (1 > 7010) Site and Sequence

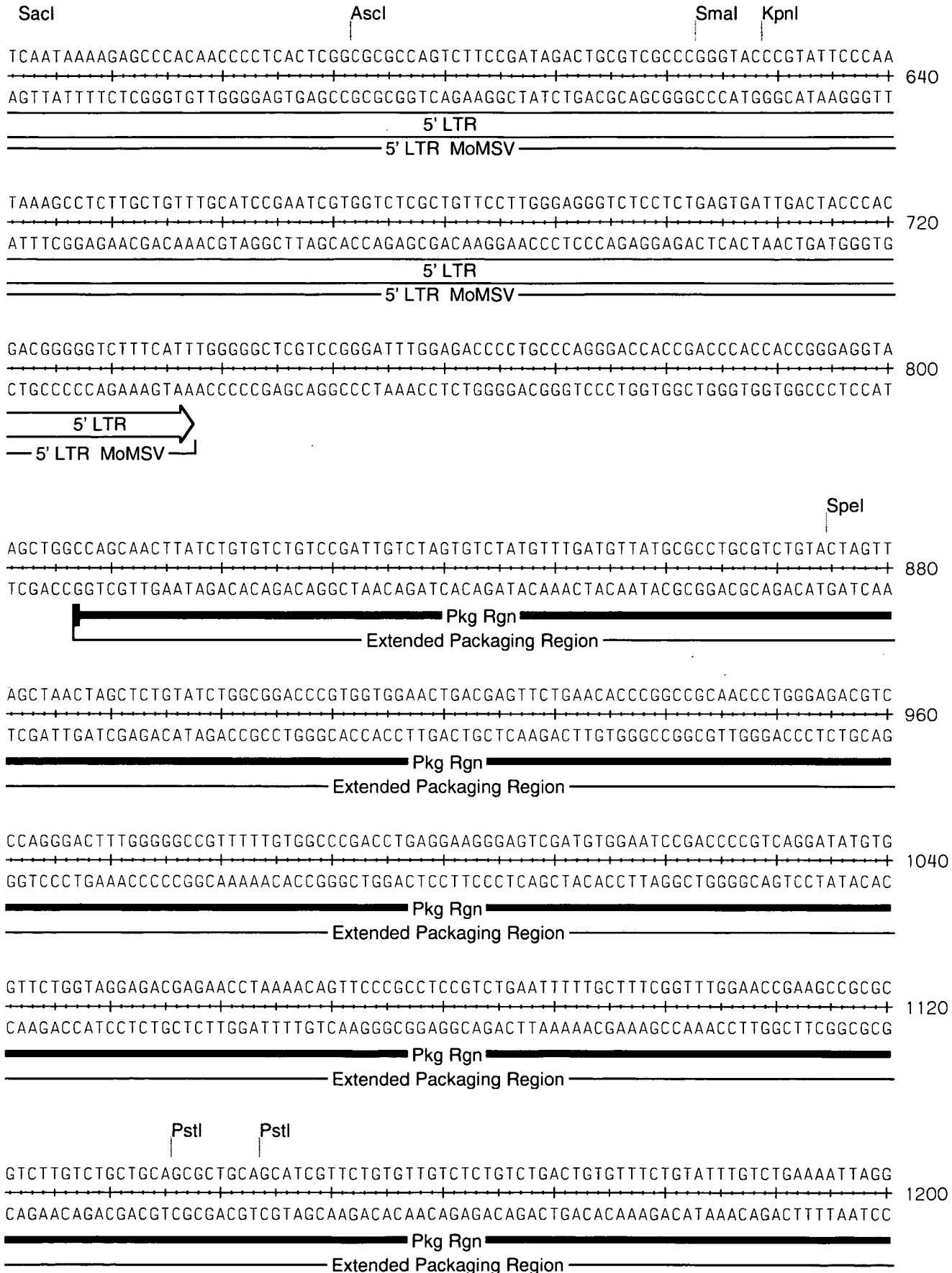


FIG. 14 (cont)

Thursday, June 13, 2002 3:42 PM

Page 3

GD2407 pLNBLV-YFP Map.MPD (1 > 7010) Site and Sequence

GCCAGACTGTTACCACTCCCTTAAGTTTGACCTTAGGTCCTGGAAGATGTCGAGCGGATCGCTCACAACCAGTCGGTA
CGGTCTGACAATGGTGAGGGAATTCAAACCTGGAATCCAGTGACCTTCTACAGCTCGCCTAGCGAGTGTGGTCAGCCAT

1280

Pkg Rgn

Extended Packaging Region

PstI

GATGTCAAGAAGAGACGTTGGGTTACCTTCTGCTCTGCAGAATGGCCAACCTTTAACGTGGATGGCCGCGAGACGGCAC
CTACAGTTCTTCTCTGCAACCCAATGGAAGACGAGACGTCTTACCGGTTGAAATTGCAGCCTACCGGCGCTCTGCCGTG

1360

Pkg Rgn

Extended Packaging Region

CTTTAACCGAGACCTCATCACCCAGGTTAAGATCAAGGTCTTTTACCTGGCCCCGATGGACACCCAGACCAGGTCCCT
GAAATTGGCTCTGGAGTAGTGGGTCCAATTCTAGTTCCAGAAAAGTGACCGGGCGTACCTGTGGGTCTGGTCCAGGGGA

1440

Pkg Rgn

Extended Packaging Region

ACATCGTGACCTGGGAAGCCTTGCTTTTGACCCCCCTCCCTGGGTCAAGCCCTTTGTACACCCTAAGCCTCCGCTCCT
TGTAGCACTGGACCTTCGGAACCGAAAACCTGGGGGAGGGACCCAGTTCCGGGAAACATGTGGGATTCCGAGGCGGAGGA

1520

Pkg Rgn

Extended Packaging Region

CTTCTCCATCCGCCCCGTCTCTCCCCCTTGAACCTCCTCGTTTCGACCCCGCCTCGATCCTCCCTTTATCCAGCCCTCAC
GAAGGAGGTAGGCGGGCAGAGAGGGGGAACCTGGAGGAGCAAGCTGGGGCGGAGCTAGGAGGGAATAGGTCGGGAGTG

1600

Pkg Rgn

Extended Packaging Region

NarI

EcoRI

BclI

TCCTTCTCTAGGCGCCGAATTCCGATCTGATCAAGAGACAGGATGAGGATCGTTTCGCATGATTGAACAAGATGGATTG
AGGAAGAGATCCGCGGCCTTAAGGCTAGACTAGTTCTCTGTCTACTCCTAGCAAAGCGTACTAAGTTGTTCTACCTAAC

1680

Pkg Rgn
Extended Packaging

Met Ile Glu Gln Asp Gly Leu
Neomycin Phosphotransferase

CACGCAGGTTCTCCGGCCGCTTGGGTGGAGAGGCTATTCCGGCTATGACTGGGCACAACAGACAATCCGGCTGCTCTGATGC
GTGCGTCCAAGAGGCCGGCGAACCCACCTCTCCGATAAGCCGATACTGACCCGTGTTGTCTGTTAGCCGACGAGACTACG

1760

His Ala Gly Ser Pro Ala Ala Trp Val Glu Arg Leu Phe Gly Tyr Asp Trp Ala Gln Gln Thr Ile Gly Cys Ser Asp Ala
Neomycin Phosphotransferase

NarI

CGCCGTGTTCCGGCTGTCAGCGCAGGGGCGCCCGGTTCTTTTTGTCAAGACCGACCTGTCCGGTGCCCTGAATGAACTGC
GCGGCACAAGGCCGACAGTCGCGTCCCCGCGGGCCAAGAAAAACAGTTCTGGCTGGACAGGCCACGGGACTTACTTGACG

1840

Ala Val Phe Arg Leu Ser Ala Gln Gly Arg Pro Val Leu Phe Val Lys Thr Asp Leu Ser Gly Ala Leu Asn Glu Leu
Neomycin Phosphotransferase



GACCAAGCGACGCCAACCTGCCATCACGAGATTTGATTCCACCGCCGCTTCTATGAAAGGTTGGGCTTCGGAATCGT 2560
CTGGTTCGCTGCGGGTTGGACGGTAGTGCTCTAAAGCTAAGGTGGCGGCGGAAGATACTTTCCAACCCGAAGCCTTAGCA

NaeI

SmaI

TTTCCGGGACGCCGGCTGGATGATCCTCCAGCGCGGGGATCTCATGCTGGAGTTCTTCGCCCACCCGGGCTCGATCCCC 2640
AAAGGCCCTGCGGCCGACCTACTAGGAGGTGCGCCCCCTAGAGTACGACCTCAAGAAGCGGGTGGGGCCCCGAGCTAGGGG

NruI

PvuII

TCGCGAGTTGGTTCAGCTGCTGCCTGAGGCTGGACGACCTCGCGGAGTTCTACCGGCAGTGCAAATCCGTCGGCATCCAG 2720
AGCGCTCAACCAAGTCGACGACGGACTCCGACCTGCTGGAGCGCTCAAGATGGCCGTACGTTTAGGCAGCCGTAGGTC

PstI

GAAACCAGCAGCGGCTATCCGCGCATCCATGCCCCGAAC TGCAGGAGTGGGGAGGCACGATGGCCGCTTTGGTCGAGGC 2800
CTTTGGTCGTCGCCGATAGGCGCGTAGGTACGGGGGCTTGACGTCTCACCCCTCCGTGCTACCGGCGAAACCAGTCCG

BamHI

GGATCCTAGCAGAAAAATAAGACTTGATTCCCCCTTAAATACAACTGCTAGAAAATGAATGGCTCTCCCGCCTTTTTT 2880
CCTAGGATCGTCTTTTTATTCTGAACCTAAGGGGGAATTTAATGTTGACGATCTTTTACTTACCGAGAGGGCGGAAAAAA

BLV Pro

BLV Promoter

NarI

PvuII

GAGGGGGAATCATTTGTATGAAAGATCATGCCGACCTAGGCGCCGCCACCGCCCCGTAAACCAGACAGAGACGTACGCTG 2960
CTCCCCCTTAGTAAACATACTTTCTAGTACGGCTGGATCCGCGCGGTTGGCGGGGCATTTGGTCTGTCTCTGCAGTCGAC

BLV Pro

BLV Promoter

PvuII

CCAGAAAAGCTGGTGACGGCAGCTGGTGGCTAGAATCCCCGTACCTCCCCAACTTCCCCTTTCCCGAAAAATCCACACCC 3040
GGTCTTTTCGACCACTGCCGTCGACCACCGATCTTAGGGGCATGGAGGGGTGAAGGGGAAAGGGCTTTTTAGGTGTGGG

BLV Pro

BLV Promoter

NaeI

TGAGCTGCTGACCTCACCTGCTGATAAATTAATAAAATGCCGGCCCTGTGAGTTAGCGGCACCAGAAGCGTTCTTCTCC 3120
ACTCGACGACTGGAGTGGACGACTATTTAATTATTTACGGCCGGGACAGCTCAATCGCCGTGGTCTTCGCAAGAAGAGG

BLV Pro

BLV Promoter



AGCGTGCAGCTCGCCGACCACTACCAGCAGAACACCCCCATCGGCGACGGCCCCGTGCTGCTGCCCCACAACCACTACCT
 TCGCACGTCGAGCGGCTGGTGATGGTCGTCTTGTGGGGGTAGCCGCTGCCGGGGCACGACGACGGGCTGTTGGTGATGGA
 Ser Val Gln Leu Ala Asp His Tyr Gln Gln Asn Thr Pro Ile Gly Asp Gly Pro Val Leu Leu Pro Asp Asn His Tyr Leu
 EYFP

GAGCTACCAGTCCGCCCTGAGCAAAGACCCCAACGAGAAGCGCGATCACATGGTCTGCTGGAGTTCGTGACCGCCGCCG
 CTCGATGGTCAGGCGGGACTCGTTTCTGGGGTTGCTCTTCGCGCTAGTGTACCAGGACGACCTCAAGCACTGGCGGGCGG
 Ser Tyr Gln Ser Ala Leu Ser Lys Asp Pro Asn Glu Lys Arg Asp His Met Val Leu Leu Glu Phe Val Thr Ala Ala
 EYFP

GGATCACTCTCGGCATGGACGAGCTGTACAAGTAAAGCGGCCGCACTCGAGATATCTAGACCCAGCTTTCTTGTACAAAG
 CCTAGTGAGAGCCGTACCTGCTCGACATGTTCAATTCGCCGGCGTGAGCTCTATAGATCTGGGTCGAAAGAACATGTTTC
 Gly Ile Thr Leu Gly Met Asp Glu Leu Tyr Lys
 EYFP attB2 attB2

Clal
 TGGTGATAACATCGATAAAATAAAAGATTTTATTTAGTCTCCAGAAAAAGGGGGAATGAAAGACCCACCTGTAGGTTT
 ACCACTATTGTAGCTATTTTATTTTCTAAAATAAATCAGAGGTCTTTTCCCCCTTACTTTCTGGGGTGGACATCCAA
 att 3' LTR 3' LTR MoMLV

NheI
 GGCAAGCTAGCTTAAGTAACGCCATTTTGAAGGCATGGAAAAATACATAACTGAGAATAGAGAAGTTCAGATCAAGGTC
 CGGTTGATCGAATTCATTGCGGTAAAACGTTCCGTACCTTTTATGTATTGACTCTTATCTCTTCAAGTCTAGTTCCAG
 3' LTR 3' LTR MoMLV

PvuII EcoRV
 AGGAACAGATGGAACAGCTGAATATGGGCCAAACAGGATATCTGTGGTAAGCAGTTCCTGCCCCGGCTCAGGGCCAAGAA
 TCCTTGCTACCTTGTCGACTTATACCCGGTTTGTCTATAGACACCATTCGTCAAGGACGGGGCCGAGTCCCGGTTCTT
 3' LTR 3' LTR MoMLV

PvuII EcoRV
 CAGATGGAACAGCTGAATATGGGCCAAACAGGATATCTGTGGTAAGCAGTTCCTGCCCCGGCTCAGGGCCAAGAACAGAT
 GTCTACCTTGTCGACTTATACCCGGTTTGTCTATAGACACCATTCGTCAAGGACGGGGCCGAGTCCCGGTTCTTGTCTA
 3' LTR 3' LTR MoMLV

FIG. 14 (cont)

Thursday, June 13, 2002 3:42 PM

Page 8

GD2407 pLNBLV-YFP Map.MPD (1 > 7010) Site and Sequence

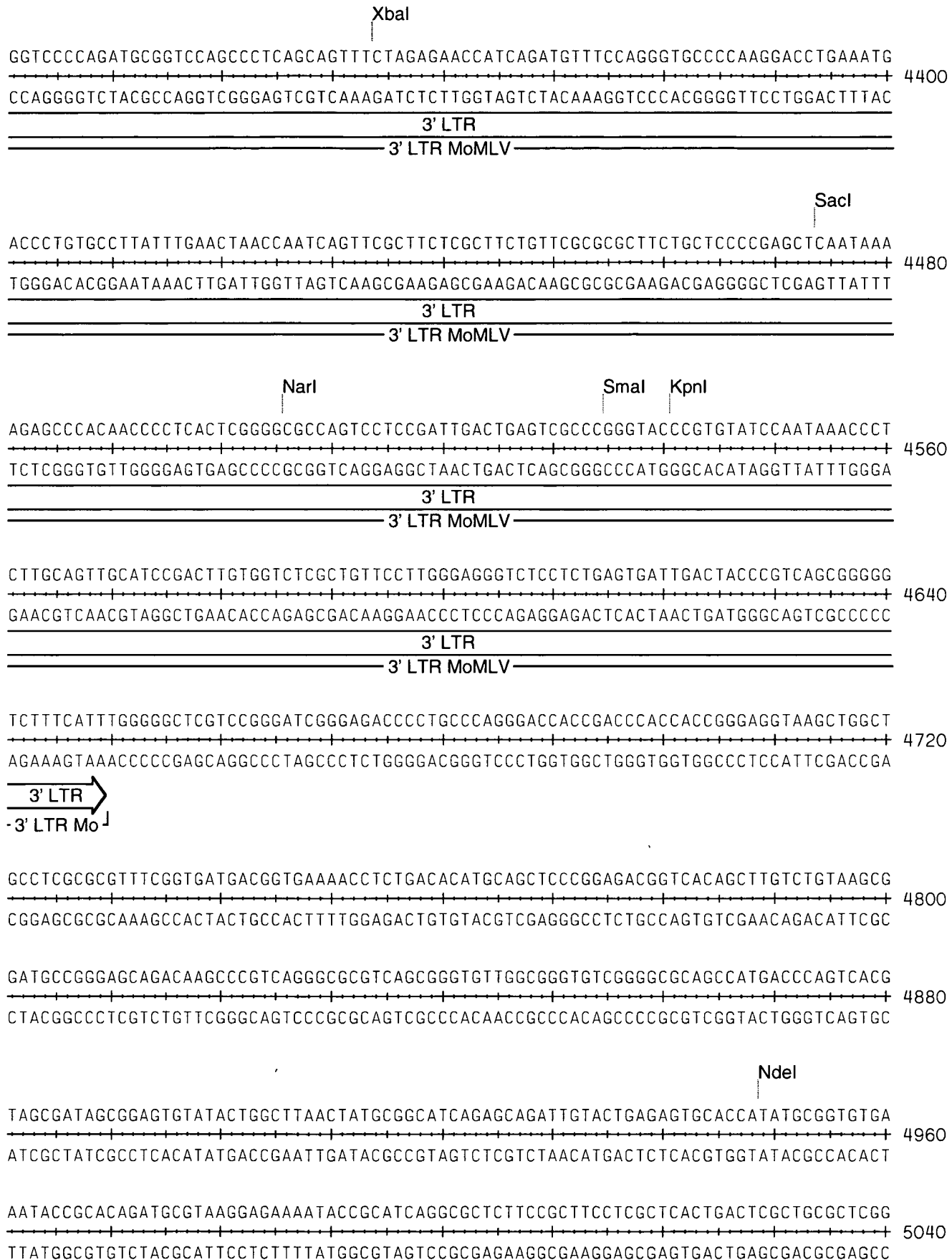


FIG. 14 (cont)

Page 9

Thursday, June 13, 2002 3:42 PM

GD2407 pNLBV-YFP Map.MPD (1 > 7010) Site and Sequence

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5120
AGCAAGCCGACGCCGCTCGCCATAGTCGAGTGAGTTTCCGCCATTATGCCAATAGGTGTCTTAGTCCCTATTGCGTCTT

AAGAACATGTGAGCAAAAGGCCAGCAAAAGGCCAGGAACCGTAAAAAGGCCGCTTGCTGGCGTTTTTTCATAGGCTCCG
5200
TTCTTGTAACACTCGTTTTCCGGTCGTTTTCCGGTCCTTGGCATTTCCTGGCGCAACGACCGCAAAAAGGTATCCGAGGC



CCCCCTGACGAGCATCAGAAAAATCGACGCTCAAGTCAGAGGTGGCGAAACCCGACAGGACTATAAAGATACCAGGCGT
5280
GGGGGGACTGCTCGTAGTGTTTTAGCTGCGAGTTCAGTCTCCACCGCTTTGGGCTGTCTGATATTTCTATGGTCCGCA

TTCCCCCTGGAAGCTCCCTCGTGCCTCTCCTGTTCCGACCCTGCCGCTTACCGGATACCTGTCCGCTTTCTCCCTTCG
5360
AAGGGGGACCTTCGAGGGAGCACGCGAGAGGACAAGGCTGGGACGGCGAATGGCCTATGGACAGGCGGAAAGAGGGAAGC

GGAAGCGTGGCGCTTTCTCATAGCTCACGCTGTAGGTATCTCAGTTCGGTGTAGGTGCTTCCGCTCCAAGCTGGGCTGTGT
5440
CCTTCGCACCGCGAAAGAGTATCGAGTGCGACATCCATAGAGTCAAGCCACATCCAGCAAGCGAGGTTCGACCCGACACA

GCACGAACCCCCGTTAGCCCGACCGCTGCGCCTTATCCGGTAACTATCGTCTTGAGTCCAACCCGGTAAGACACGACT
5520
CGTGCTTGGGGGGCAAGTCGGGCTGGCGACGCGAATAGGCCATTGATAGCAGAACTCAGGTTGGGCCATTCTGTGCTGA

TATCGCCACTGGCAGCAGCCACTGGTAACAGGATTAGCAGAGCGAGGTATGTAGGCGGTGCTACAGAGTTCTTGAAGTGG
5600
ATAGCGGTGACCGTCGTCGGTGACCATTTGTCTAATCGTCTCGCTCCATACATCCGCCACGATGTCTCAAGAACTTCACC

TGGCCTAACTACGGCTACACTAGAAGGACAGTATTTGGTATCTGCGCTCTGCTGAAGCCAGTTACCTTCGGAAAAAGAGT
5680
ACCGGATTGATGCCGATGTGATCTTCTGTCTATAAACCATAGACGCGAGACGACTTCGGTCAATGGAAGCCTTTTCTCA

TGGTAGCTCTTGATCCGGCAAAACAAACCACCGCTGGTAGCGGTGGTTTTTTTGTGTTGCAAGCAGCAGATTACGCGCAGAA
5760
ACCATCGAGAACTAGGCCGTTTGTGTTGGTGGCGACCATCGCCACCAAAAAACAAACGTTTCGTCTAATGCGCGTCTT

AAAAAGGATCTCAAGAAGATCCTTTGATCTTTTCTACGGGTCTGACGCTCAGTGAACGAAAACACGTTAAGGGATT
5840
TTTTTCTAGAGTTCTTCTAGGAACTAGAAAAGATGCCCCAGACTGCGAGTCACCTTGCTTTTGAGTGCAATTCCTAA

BspHI

DraI

DraI

TTGGTCATGAGATTATCAAAAAGGATCTTCACCTAGATCCTTTTAAATTAATAATGAAGTTTTAAATCAATCTAAAGTAT
5920
AACCAGTACTCTAATAGTTTTTCTAGAAAGTGGATCTAGGAAAATTAATTTTTACTTCAAATTTAGTTAGATTTTCATA

ATATGAGTAACTTGGTCTGACAGTTACCAATGCTTAATCAGTGAGGCACCTATCTCAGCGATCTGTCTATTTTCGTTTCAT
6000
TATACTCATTTGAACCAGACTGTCAATGGTTACGAATTAGTCACTCCGTGGATAGAGTCGCTAGACAGATAAAGCAAGTA

• Trp His Lys Ile Leu Ser Ala Gly Ile Glu Ala Ile Gln Arg Asn Arg Glu Asp
b-Lactamase

Thursday, June 13, 2002 3:42 PM

GD2407 pLNBLV-YFP Map.MPD (1 > 7010) Site and Sequence

CCATAGTTGCCTGACTCCCCGTCGTGTAGATAACTACGATACGGGAGGGCTTACCATCTGGCCCCAGTGCTGCAATGATA
 6080
 GGTATCAACGGACTGAGGGGCGAGCACATCTATTGATGCTATGCCCTCCGAATGGTAGACCGGGTCACGACGTTACTAT
 Met Thr Ala Gln Ser Gly Thr Thr Tyr Ile Val Val Ile Arg Ser Pro Lys Gly Asp Pro Gly Leu Ala Ala Ile Ile
 b-Lactamse

CCGCGAGACCCACGCTCACCGGCTCCAGATTTATCAGCAATAAACCAGCCAGCCGAAGGGCCGAGCGCAGAAGTGGTCC
 6160
 GGGCTCTGGGTGCGAGTGCGCGAGGTCTAAATAGTCGTTATTTGGTCGGTCGGCCTTCCCGGCTCGCGTCTTACCAGG
 Gly Arg Ser Gly Arg Glu Gly Ala Gly Ser Lys Asp Ala Ile Phe Trp Gly Ala Pro Leu Ala Ser Arg Leu Leu Pro Gly
 b-Lactamse

TGCAACTTTATCCGCTCCATCCAGTCTATTAATTGTTGCCGGGAAGCTAGAGTAAGTAGTTCGCCAGTTAATAGTTTGC
 6240
 ACGTTGAAATAGGCGGAGGTAGGTCAGATAATTAACAACGGCCCTTCGATCTCATTTCATCAAGCGGTCAATTATCAAACG
 Ala Val Lys Asp Ala Glu Met Trp Asp Ile Leu Gln Gln Arg Ser Ala Leu Thr Leu Leu Glu Gly Thr Leu Leu Lys Arg
 b-Lactamse

GCAACGTTGTTGCCATTGCTGCAGGCATCGTGGTGTACGCTCGTCGTTTGGTATGGCTTCATTTCAGCTCCGGTTCCTCAA
 6320
 CGTTGCAACAACGGTAACGACGTCCGTAGCACCACAGTGCAGAGCAGCAAACCATACCGAAGTAAGTCGAGGCCAAGGGTT
 Leu Thr Thr Ala Met Ala Ala Pro Met Thr Thr Asp Arg Glu Asp Asn Pro Ile Ala Glu Asn Leu Glu Pro Glu Trp
 b-Lactamse

CGATCAAGGCGAGTTACATGATCCCCATGTTGTGCAAAAAAGCGGTTAGCTCCTTCGGTCCTCCGATCGTTGTGAGAAG
 6400
 GCTAGTTCCGCTCAATGTACTAGGGGGTACAACACGTTTTTTTCGCCAATCGAGGAAGCCAGGAGGCTAGCAACAGTCTTC
 Arg Asp Leu Arg Thr Val His Asp Gly Met Asn His Leu Phe Ala Thr Leu Glu Lys Pro Gly Gly Ile Thr Thr Leu Leu
 b-Lactamse

TAAGTTGGCCGAGTGTTATCACTCATGGTTATGGCAGCACTGCATAATTCTCTTACTGTCATGCCATCCGTAAGATGCT
 6480
 ATTCAACCGGCGTCACAATAGTGAGTACCAATACCGTCGTGACGTATTAAGAGAATGACAGTACGGTAGGCATTCTACGA
 Leu Asn Ala Ala Thr Asn Asp Ser Met Thr Ile Ala Ala Ser Cys Leu Glu Arg Val Thr Met Gly Asp Thr Leu His Lys
 b-Lactamse

TTTCTGTGACTGGTGAGTACTCAACCAAGTCATTCTGAGAATAGTGTATGCGGCGACCGAGTTGCTCTTGCCCGGCGTCA
 6560
 AAAGACACTGACCACTCATGAGTTGGTTTCAGTAAGACTCTTATCACATACGCCGCTGGCTCAACGAGAAGGGCCGCGAGT
 Glu Thr Val Pro Ser Tyr Glu Val Leu Asp Asn Gln Ser Tyr His Ile Arg Arg Gly Leu Gln Glu Gln Gly Ala Asp
 b-Lactamse

ACACGGGATAATACCGCGCCACATAGCAGAACTTTAAAAGTGCTCATTCATTGGAAAACGTTCTTCGGGGCGAAAACCTCTC
 6640
 TGTGCCCTATTATGGCGCGGTGTATCGTCTTGAAATTTTCACGAGTAGTAACCTTTTGCAAGAAGCCCCGCTTTTGAGAG
 Val Arg Ser Leu Val Ala Gly Cys Leu Leu Val Lys Phe Thr Ser Met Met Pro Phe Arg Glu Glu Pro Arg Phe Ser Glu
 b-Lactamse

Thursday, June 13, 2002 3:42 PM

GD2407 pLNBLV-YFP Map.MPD (1 > 7010) Site and Sequence

AAGGATCTTACCGCTGTTGAGATCCAGTTCGATGTAACCCACTCGTGCACCCAACTGATCTTCAGCATCTTTTACTTTCA
 TTCCTAGAATGGCGACAACCTCTAGGTCAAGCTACATTGGGTGAGCACGTGGGTTGACTAGAAGTCGTAGAAAATGAAAGT
 Leu Ile Lys Gly Ser Asn Leu Asp Leu Glu Ile Tyr Gly Val Arg Ala Gly Leu Gln Asp Glu Ala Asp Lys Val Lys Val
 b-Lactamse

CCAGCGTTTCTGGGTGAGCAAAAACAGGAAGGCAAAATGCCGCAAAAAAGGGAATAAGGGCGACACGGAAATGTTGAATA
 GGTGCGAAAGACCCACTCGTTTTTGTCTTCCGTTTTACGGCGTTTTTCCCTTATTCCCGCTGTGCCTTTACAACCTTAT
 Leu Thr Glu Pro His Ala Phe Val Pro Leu Cys Phe Ala Ala Phe Phe Pro Ile Leu Ala Val Arg Phe His Gln Ile
 b-Lactamse

BspHI

CTCATACTCTTCTTTTTCAATATTATTGAAGCATTTATCAGGGTTATTGTCTCATGAGCGGATACATATTTGAATGTAT
 GAGTATGAGAAGGAAAAAGTTATAATAACTTCGTAAATAGTCCCAATAACAGAGTACTCGCCTATGTATAAACTTACATA

Ser Met
 -b-Lac

BspHI

TTAGAAAAATAAACAAATAGGGGTTCGCGCACATTTCCCCGAAAAGTGCCACCTGACGTCTAAGAAACCATTATTATCA
 AATCTTTTTATTGTTTATCCCCAAGGCGCGTGTAAGGGGCTTTTCACGGTGGACTGCAGATTCTTTGGTAATAATAGT

TGACATTAACCTATAAAAAATAGGCGTATCACGAGGCCCTTTTCGTCTTCAA
 ACTGTAATTGGATATTTTTATCCGCATAGTGCTCCGGGAAAGCAGAAGTT 7010

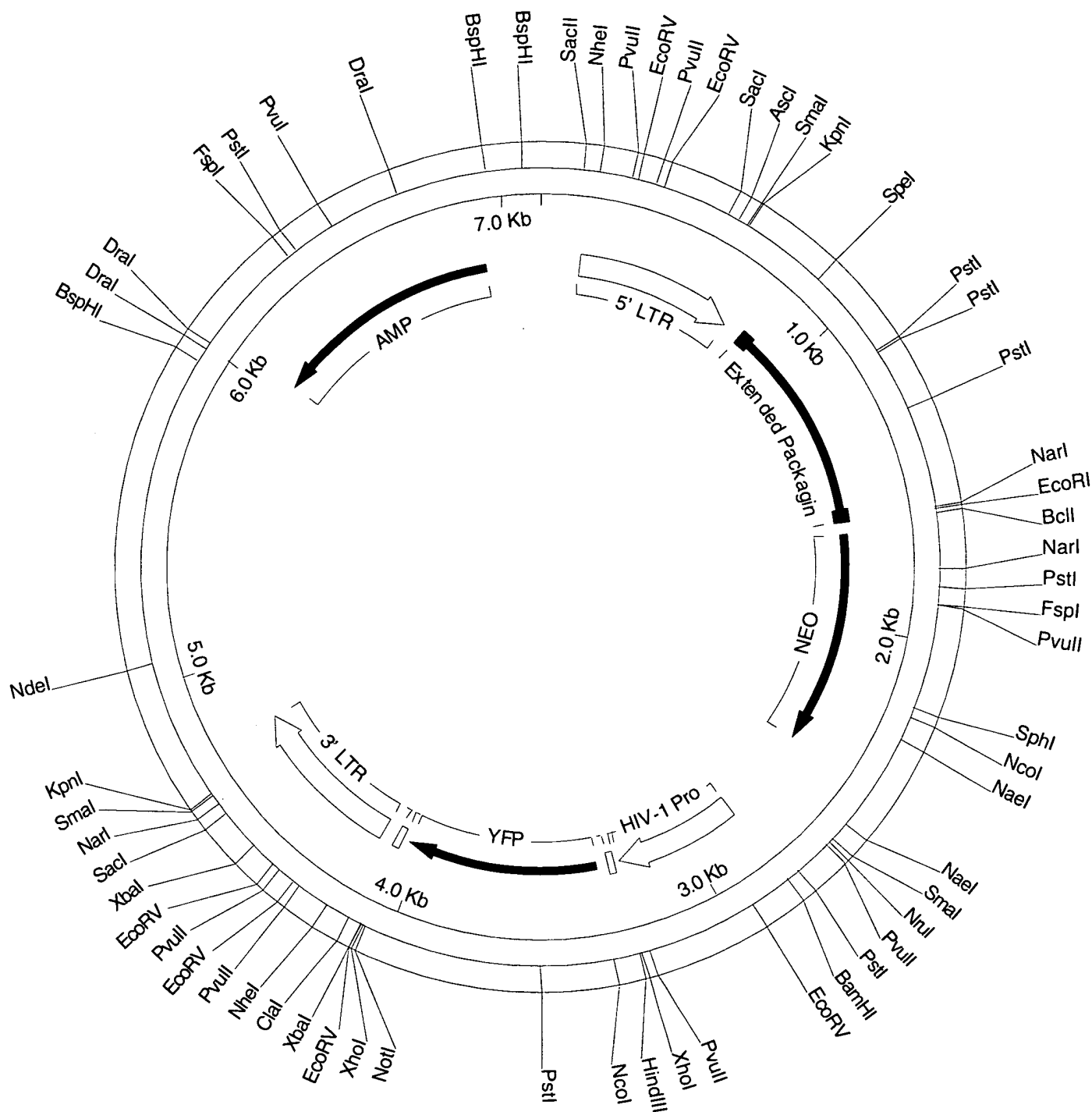


FIG. 15

FIG. 16

Page 1

Tuesday, July 02, 2002 2:11 PM

pLNHiv-YFP Map.MPD (1 > 7121) Site and Sequence

Enzymes : 36 of 538 enzymes (Filtered)

Settings : Circular, Certain Sites Only, Standard Genetic Code

GAATTAATTCATACCAGATACCCGAAAACGTGCTCTCCAAATGTGTCCCCCTCACACTCCCAAATTCGCGGGCTTCTGCCT
CTTAATTAAGTATGGTCTAGTGGCTTTTGACAGGAGGTTTACACAGGGGGAGTGTGAGGGTTTAAGCGCCCGAAGACGGA

SacII

CTTAGACCACTCTACCCTATTCCCCACACTCACCGGAGCCAAAGCCGCGGCCCTTCCGTTTCTTTGCTTTTGAAAGACCC
GAATCTGGTGAGATGGGATAAGGGGTGTGAGTGGCCTCGGTTTCGGCGCCGGAAGGCAAAGAAACGAAAACTTTCTGGG

5' LTR

NheI

CACCCGTAGGTGGCAAGCTAGCTTAAGTAACGCCACTTTGCAAGGCATGGAAAAATACATAACTGAGAATAGAAAAGTTC
GTGGGCATCCACCGTTCGATCGAATTCATTGCGGTGAAACGTTCCGTACCTTTTTATGTATTGACTCTTATCTTTTCAAG

5' LTR

PvuII

EcoRV

AGATCAAGGTCAGGAACAAAGAAACAGCTGAATACCAAACAGGATATCTGTGGTAAGCGGTTCTTGCCCCGGCTCAGGGC
TCTAGTTCCAGTCCTTGTTTCTTTGTGCACTTATGGTTTGTCTATAGACACCATTCGCCAAGGACGGGGCCGAGTCCCG

5' LTR

PvuII

EcoRV

CAAGAACAGATGAGACAGCTGAGTGATGGGCCAAACAGGATATCTGTGGTAAGCAGTTCTTGCCCCGGCTCGGGGCCAAG
GTTCTTGTCTACTCTGTGCACTCACTACCCGGTTTGTCTATAGACACCATTCGTCAAGGACGGGGCCGAGCCCCGGTTC

5' LTR

AACAGATGGTCCCCAGATGCGGTCCAGCCCTCAGCAGTTTCTAGTGAATCATCAGATGTTTCCAGGGTGCCCCAAGGACC
TTGTCTACCAGGGGTCTACGCCAGGTGCGGAGTCGTCAAAGATCACTTAGTAGTCTACAAAGGTCCACGGGGTTTCTGG

5' LTR

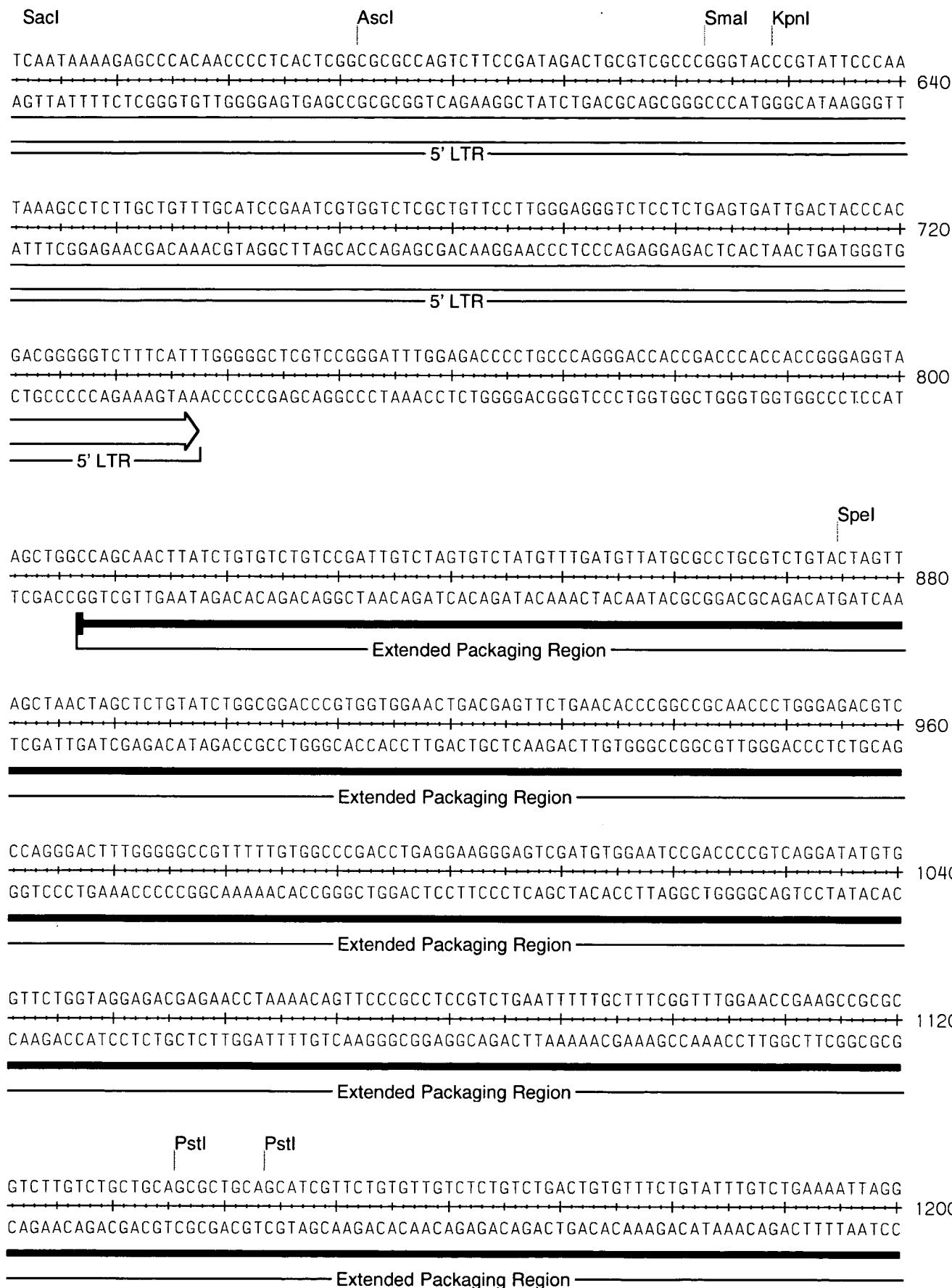
TGAAAATGACCCTGTACCTTATTTGAACTAACCAATCAGTTCGCTTCTCGCTTCTGTTTCGCGCGCTTCCGCTCTCCGAGC
ACTTTTACTGGGACATGGAATAAACTTGATTGGTTAGTCAAGCGAAGAGCGAAGACAAGCGCGGAAGCGGAGAGGCTCG

5' LTR

FIG. 16 (cont)

Tuesday, July 02, 2002 2:11 PM
pLNHiv-YFP Map.MPD (1 > 7121) Site and Sequence

Page 2



Tuesday, July 02, 2002 2:11 PM
pLNHiv-YFP Map.MPD (1 > 7121) Site and Sequence

GCCAGACTGTTACCACTCCCTTAAGTTTGACCTTAGGTCCTGGAAGATGTCGAGCGGATCGCTCACAACCAGTCGGTA
CGGTCTGACAATGGTGAGGAATTCAAACCTGGAATCCAGTGACCTTTCTACAGCTCGCCTAGCGAGTGTGGTCAGCCAT

1280

Extended Packaging Region

PstI

GATGTCAAGAAGAGACGTTGGGTTACCTTCTGCTCTGCAGAATGGCCAACCTTTAACGTGGATGGCCGCGAGACGGCAC
CTACAGTTCTTCTCTGCAACCAATGGAAGACGAGACGTCTTACCGGTTGAAATTGCAGCCTACCGGCGCTCTGCCGTG

1360

Extended Packaging Region

CTTTAACCGAGACCTCATCACCCAGGTTAAGATCAAGGTCTTTTACCTGGCCCCGCATGGACACCCAGACCAGGTCCCT
GAAATTGGCTCTGGAGTAGTGGGTCCAATTCTAGTTCCAGAAAAGTGACCGGGCGTACCTGTGGGTCTGGTCCAGGGGA

1440

Extended Packaging Region

ACATCGTGACCTGGGAAGCCTTGGCTTTTGACCCCCCTCCCTGGGTCAAGCCCTTTGTACACCCTAAGCCTCCGCTCCT
TGTAGCACTGGACCTTCGGAACCGAAAACCTGGGGGAGGGACCCAGTTCGGGAAACATGTGGGATTTCGGAGCGGAGGA

1520

Extended Packaging Region

CTTCCTCCATCCGCCCCGTCTCTCCCCCTTGAACCTCCTCGTTGACCCCGCCTCGATCCTCCCTTTATCCAGCCCTCAC
GAAGGAGGTAGGCGGGGCAGAGAGGGGGAACCTTGGAGGAGCAAGCTGGGGCGGAGCTAGGAGGGAATAGGTCTGGGAGTG

1600

Extended Packaging Region

NarI EcoRI BclI

TCCTTCTCTAGGCGCCGAATTCCGATCTGATCAAGAGACAGGATGAGGATCGTTTCGCATGATTGAACAAGATGGATTG
AGGAAGAGATCCGCGGCCTTAAGGCTAGACTAGTTCTCTGTCTACTCCTAGCAAAGCGTACTAATTGTTCTACCTAAC

1680

Extended Packaging

Met Ile Glu Gln Asp Gly Leu
NEO

CACGCAGGTTCTCCGGCCGCTTGGGTGGAGAGGCTATTCCGCTATGACTGGGCACAACAGACAATCCGCTGCTCTGATGC
GTGCGTCCAAGAGCCGCGGAACCCACCTCTCCGATAAGCCGATACTGACCCGTGTTGTCTGTTAGCCGACGAGACTACG

1760

His Ala Gly Ser Pro Ala Ala Trp Val Glu Arg Leu Phe Gly Tyr Asp Trp Ala Gln Gln Thr Ile Gly Cys Ser Asp Ala
NEO

NarI

CGCCGTGTTCCGGCTGTCAGCGCAGGGGCGCCGGTCTTTTTGTCAAGACCGACCTGTCCGGTGCCCTGAATGAACTGC
GCGGCACAAGGCCGACAGTCGCGTCCCCGCGGGCCAAGAAAAACAGTTCTGGCTGGACAGGCCACGGGACTTACTTGACG

1840

Ala Val Phe Arg Leu Ser Ala Gln Gly Arg Pro Val Leu Phe Val Lys Thr Asp Leu Ser Gly Ala Leu Asn Glu Leu
NEO

Tuesday, July 02, 2002 2:11 PM
pLNHiv-YFP Map.MPD (1 > 7121) Site and Sequence

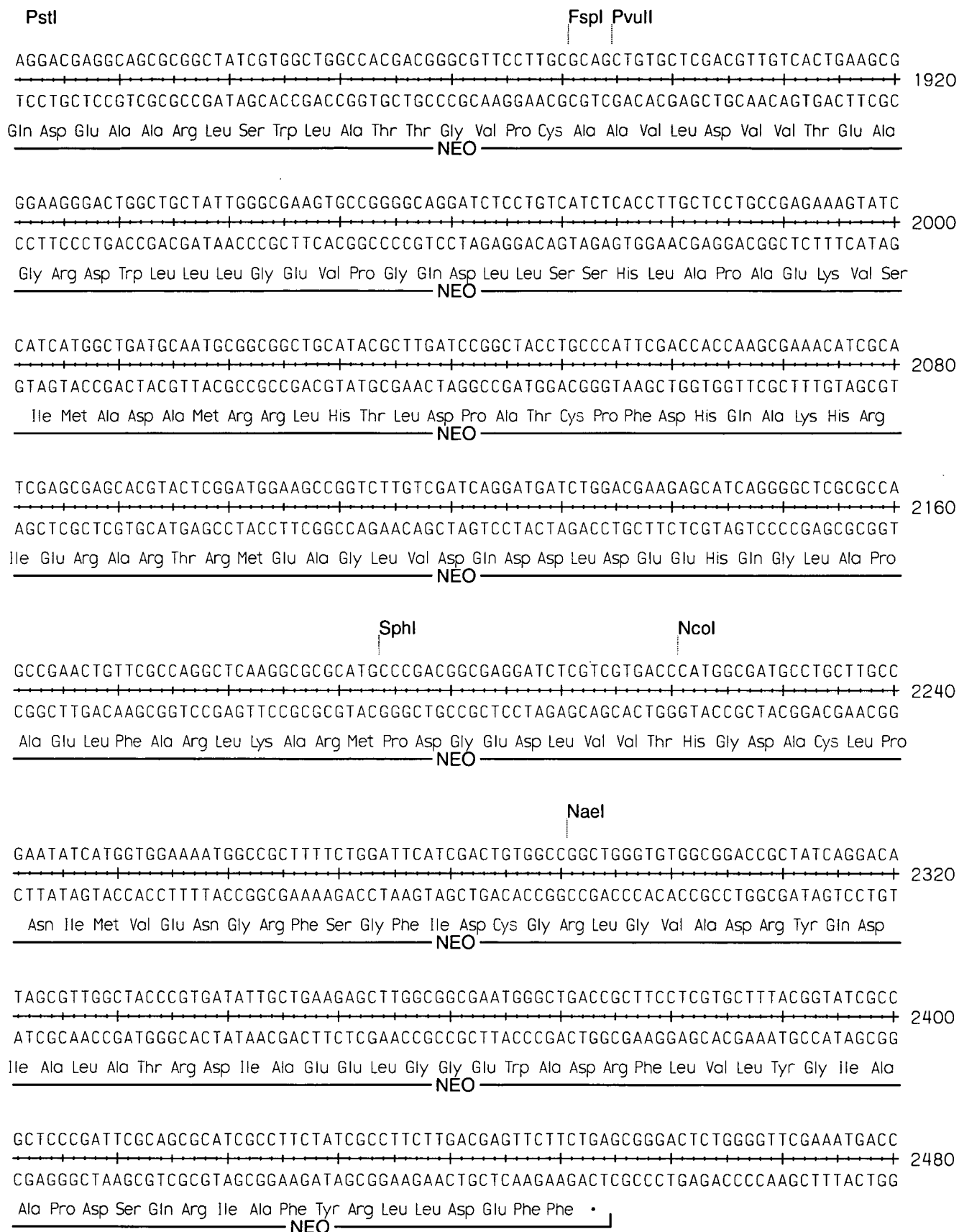


FIG. 16 (cont)

Tuesday, July 02, 2002 2:11 PM
pLNHiv-YFP Map.MPD (1 > 7121) Site and Sequence

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CTGGTTCGCTGCGGGTTGGACGGTAGTGCTCTAAAGCTAAGGTGGCGGCGGAAGATACTTTCCAACCCGAAGCCTTAGCA

NaeI

SmaI

TTTCCGGGACGCCGGCTGGATGATCCTCCAGCGCGGGATCTCATGCTGGAGTTCTTCGCCCACCCGGGCTCGATCCCC 2640
AAAGGCCCTGCGGCCGACCTACTAGGAGGTGCGGCCCTAGAGTACGACCTCAAGAAGCGGTGGGGCCCCGAGCTAGGGG

NruI

PvuII

TCGCGAGTTGGTTCAGCTGCTGCCTGAGGCTGGACGACCTCGCGGAGTTCTACCGGCAGTGCAAATCCGTCGGCATCCAG 2720
AGCGCTCAACCAAGTCGACGACGGACTCCGACCTGCTGGAGCGCTCAAGATGGCCGTACGTTTAGGCAGCCGTAGGTC

PstI

GAAACCAGCAGCGGCTATCCGCGCATCCATGCCCCGAAGTGCAGGAGTGGGAGGCACGATGGCCGCTTTGGTCGAGGC 2800
CTTTGGTCGTCGCCGATAGGCGCGTAGGTACGGGGGCTTGACGTCTCACCCCTCCGTGCTACCGGCGAAACCAGCTCCG

BamHI

GGATCCTGGAAGGGCTAATTTGGTCCCAAAGAAGACAAGAGATCCTTGATCTGTGGATCTACCACACACAAGGCTACTTC 2880
CCTAGGACCTTCCCGATTAAACCAGGGTTTCTTCTGTTCTCTAGGAAGTAGACACCTAGATGGTGTGTGTTCGATGAAG

HIV-1 Promoter

EcoRV

CCTGATTGGCAGAATTACACACCAGGGCCAGGGATCAGATATCCACTGACCTTTGGATGGTGCTTCAAGCTAGTACCACT 2960
GGACTAACCCTCTTAATGTGTGGTCCCGGTCCCTAGTCTATAGGTGACTGGAAACCTACCACGAAGTTCGATCATGGTCA

HIV-1 Promoter

TGAGCCAGAGAAGGTAGAAGAGGCCAATGAAGGAGAGACAACAGCTTGTTACACCCTATGAGCCTGCATGGGATGGAGG 3040
ACTCGGTCTCTTCCATCTTCTCCGGTACTTCTCTCTTGTGTGCAACAATGTGGGATACTCGGACGTACCCTACCTCC

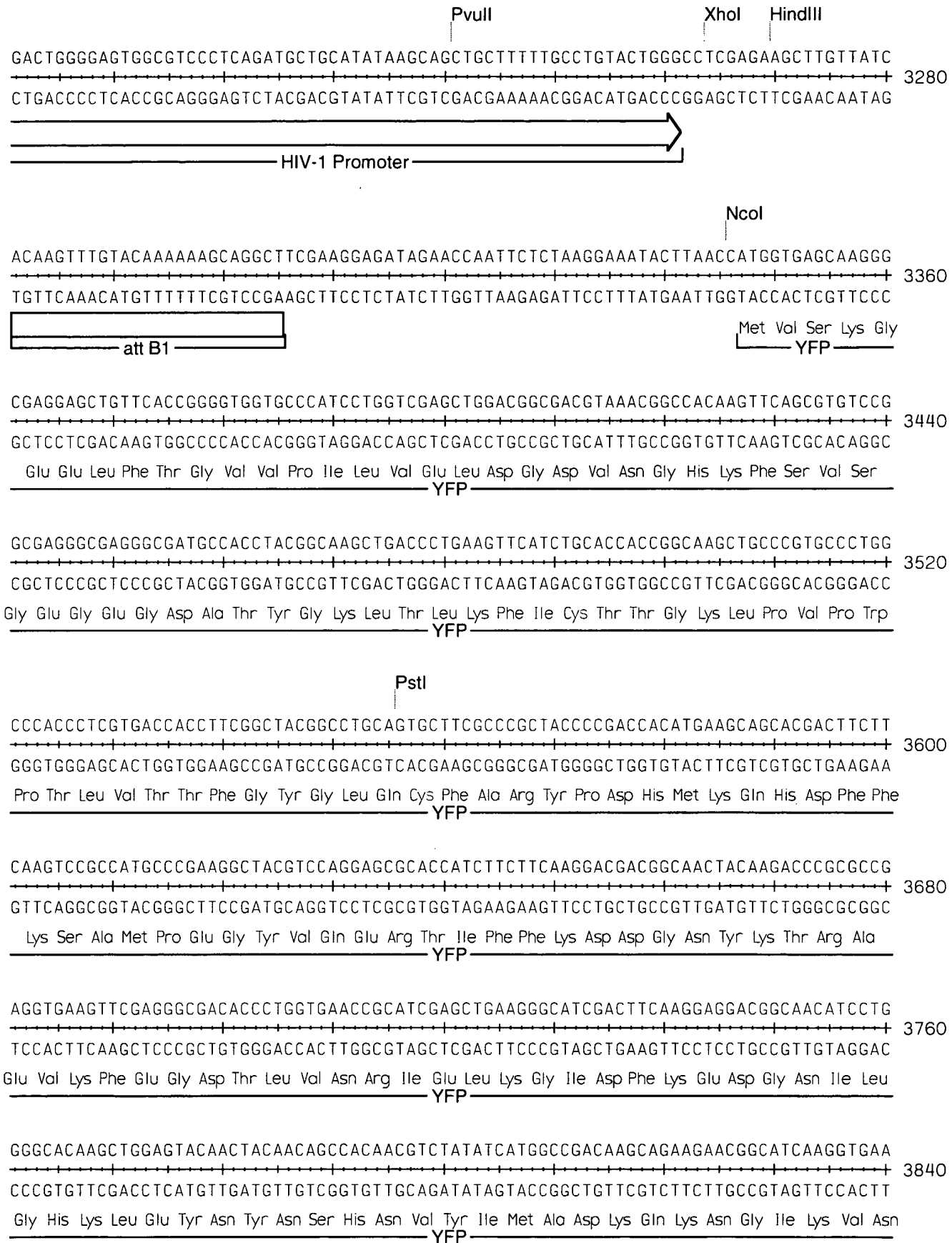
HIV-1 Promoter

ACGCGGAGAAAGAAGTGTTAGTGTGGAGGTTTGACAGCAAAGTAGCATTTTCATCACATGGCCCGAGAGCTGCATCCGGAG 3120
TGCGCCTCTTTCTTCAATCACACCTCCAAAGTGTGTTGATCGTAAAGTAGTGTACCGGGCTCTCGACGTAGGCCTC

HIV-1 Promoter

TACTACAAAGACTGCTGACATCGAGCTTTCTACAAGGGACTTTCCGCTGGGGACTTTCCAGGGAGGCGTGGCCTGGGCGG 3200
ATGATGTTTCTGACGACTGTAGCTCGAAAGATGTTCCCTGAAAGGCGACCCCTGAAAGGTCCCTCCGCACCGGACCCGCC

HIV-1 Promoter



Tuesday, July 02, 2002 2:11 PM
pLNHiv-YFP Map.MPD (1 > 7121) Site and Sequence

CTTCAAGATCCGCCACAACATCGAGGACGGCAGCGTGCAGCTCGCCGACCACTACCAGCAGAACACCCCATCGGCGACG
+-----+-----+-----+-----+-----+-----+-----+-----+-----+-----+ 3920
GAAGTTCTAGGCGGTGTTGTAGCTCCTGCCGTGCACGTCGAGCGGCTGGTGATGGTCGTCTTGTGGGGGTAGCCGCTGC
Phe Lys Ile Arg His Asn Ile Glu Asp Gly Ser Val Gln Leu Ala Asp His Tyr Gln Gln Asn Thr Pro Ile Gly Asp
-----YFP-----

GCCCCGTGCTGCTGCCCGACAACCACTACCTGAGCTACCAGTCCGCCCTGAGCAAAGACCCCAACGAGAAGCGCGATCAC
+-----+-----+-----+-----+-----+-----+-----+-----+-----+-----+ 4000
CGGGGCACGACGACGGGCTGTTGGTGATGGACTCGATGGTCAGGCGGGACTCGTTTCTGGGGTTGCTCTTCGCGCTAGTG
Gly Pro Val Leu Leu Pro Asp Asn His Tyr Leu Ser Tyr Gln Ser Ala Leu Ser Lys Asp Pro Asn Glu Lys Arg Asp His
-----YFP-----

ATGGTCCTGCTGGAGTTCGTGACCGCCGCCGGGATCACTCTCGGCATGGACGAGCTGTACAAGTAAAGCGGCCGCACTCG
+-----+-----+-----+-----+-----+-----+-----+-----+-----+-----+ 4080
TACCAGGACGACCTCAAGCACTGGCGGGCGGCCCTAGTGAGAGCCGTACCTGCTCGACATGTTCAATTCGCCGCGTGAGC
Met Val Leu Leu Glu Phe Val Thr Ala Ala Gly Ile Thr Leu Gly Met Asp Glu Leu Tyr Lys
-----YFP-----

EcoRV
XbaI

Clal

AGATATCTAGACCCAGCTTTCTTGTACAAAGTGGTGATAACATCGATAAAATAAAAGATTTTATTTAGTCTCCAGAAAAA
+-----+-----+-----+-----+-----+-----+-----+-----+-----+-----+ 4160
TCTATAGATCTGGGTCGAAAGAACATGTTTACCACACTATTGTAGCTATTTTATTTTCTAAATAAATCAGAGGTCTTTTT
[]
-----att B2-----

NheI

GGGGGAATGAAAGACCCACCTGTAGGTTTGGCAAGCTAGCTTAAGTAACGCCATTTTGAAGGCATGGAAAAATACAT
+-----+-----+-----+-----+-----+-----+-----+-----+-----+-----+ 4240
CCCCCTTACTTTCTGGGGTGGACATCCAAACGTTTCGATCGAATTCATTGCGGTAAAACGTTCCGTACCTTTTTATGTA
[]
-----3' LTR-----

PvuII

EcoRV

AACTGAGAATAGAGAAGTTCAGATCAAGGTCAGGAACAGATGGAACAGCTGAATATGGGCCAAACAGGATATCTGTGGTA
+-----+-----+-----+-----+-----+-----+-----+-----+-----+-----+ 4320
TTGACTCTTATCTCTCAAGTCTAGTTCAGTCCTTGTCTACCTTGTCGACTTATACCCGGTTTGTCTATAGACACCAT
[]
-----3' LTR-----

PvuII

EcoRV

AGCAGTTCCTGCCCCGGCTCAGGGCCAAGAACAGATGGAACAGCTGAATATGGGCCAAACAGGATATCTGTGGTAAGCAG
+-----+-----+-----+-----+-----+-----+-----+-----+-----+-----+ 4400
TCGTCAAGGACGGGGCCGAGTCCCGTTCTTGTCTACCTTGTCGACTTATACCCGGTTTGTCTATAGACACCATTCGTC
[]
-----3' LTR-----

FIG. 16 (cont)

Tuesday, July 02, 2002 2:11 PM
pLNHiv-YFP Map.MPD (1 > 7121) Site and Sequence

Page 8

XbaI

TTCTGCCCCGGCTCAGGGCCAAGAACAGATGGTCCCCAGATGCGGTCCAGCCCTCAGCAGTTTCTAGAGAACCATCAGA 4480
AAGGACGGGGCCGAGTCCCGGTTCTTGTCTACCAGGGGTCTACGCCAGGTCGGGAGTCGTCAAAGATCTCTTGGTAGTCT

3' LTR

TGTTTCCAGGGTGCCCCAAGGACCTGAAATGACCCTGTGCCTTATTTGAACTAACCAATCAGTTCGCTTCTCGCTTCTGT 4560
ACAAAGGTCCACGGGGTTCCTGGACTTTACTGGGACACGGAATAAACTTGATTGGTTAGTCAAGCGAAGAGCGAAGACA

3' LTR

SacI NarI

TCGCGCGCTTCTGCTCCCCGAGCTCAATAAAAGAGCCACAACCCCTCACTCGGGGCGCCAGTCCTCCGATTGACTGAGT 4640
AGCGCGCAAGACGAGGGGCTCGAGTTATTTCTCGGGTGTGGGGAGTGAGCCCCGCGGTCAGGAGGCTAACTGACTCA

3' LTR

SmaI KpnI

CGCCCGGGTACCCGTGTATCCAATAAACCCCTCTTGCAGTTGCATCCGACTTGTGGTCTCGCTGTTTCCTTGGGAGGGTCTC 4720
GCGGGCCCATGGGCACATAGGTTATTTGGGAGAACGTCAACGTAGGCTGAACACCAGAGCGACAAGGAACCCCTCCAGAG

3' LTR

CTCTGAGTGATTGACTACCCGTCAGCGGGGGTCTTTCATTTGGGGGCTCGTCCGGGATCGGGAGACCCCTGCCAGGGAC 4800
GAGACTCACTAACTGATGGGCAGTCGCCCCAGAAAGTAAACCCCGAGCAGGCCCTAGCCCTCTGGGGACGGGTCCCTG

3' LTR

CACCGACCCACCACGGGAGGTAAGCTGGCTGCCTCGCGGTTTTCGGTGATGACGGTGAAAACCTCTGACACATGCAGCT 4880
GTGGCTGGGTGGCCCTCCATTGACCGACGGAGCGCGCAAAGCCACTACTGCCACTTTTGGAGACTGTGTACGTCTGA

CCCGGAGACGGTCACAGCTTGTCTGTAAGCGGATGCCGGGAGCAGACAAGCCCGTCAGGGCGCGTCAGCGGGTGTGGCG 4960
GGGCCTCTGCCAGTGTGAACAGACATTGCCTACGGCCCTCGTCTGTTTCGGGCAGTCCCGCGCAGTCGCCACAACCGC

GGTGTGGGGGCGCAGCCATGACCCAGTCACGTAGCGATAGCGGAGTGTATACTGGCTTAACCTATGCGGCATCAGAGCAGA 5040
CCACAGCCCCGCGTCGGTACTGGGTCACTGCATCGCTATCGCCTCACATATGACCGAATTGATACGCCGTAGTCTCGTCT

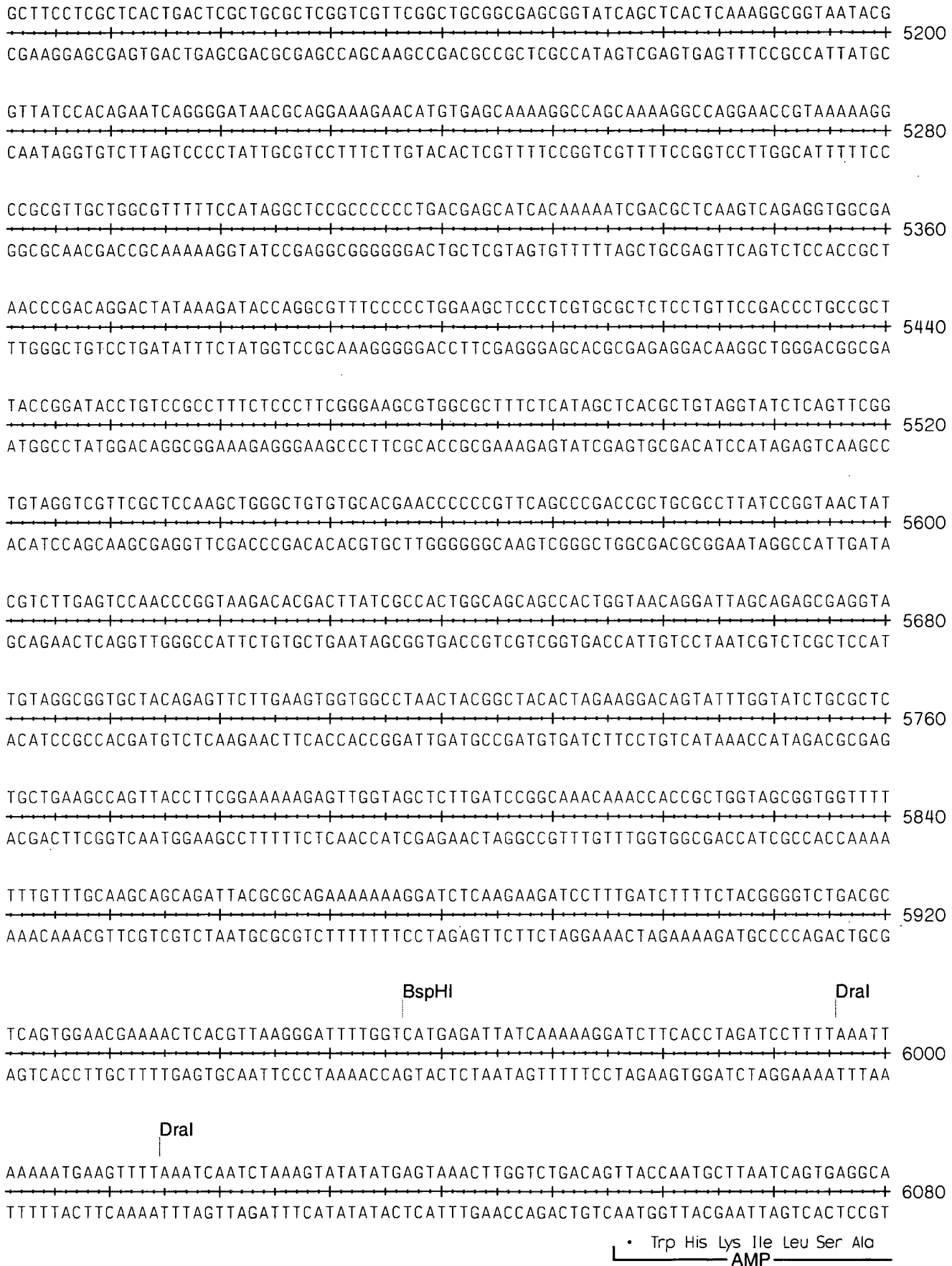
NdeI

TTGTACTGAGAGTGACCATATGCGGTGTGAAATACCGCACAGATGCGTAAGGAGAAAATACCGCATCAGGCGCTCTTCC 5120
AACATGACTCTCACGTGGTATACGCCACACTTTATGGCGTGTCTACGCATTCTCTTTTATGGCGTAGTCCGCGAGAAGG

FIG. 16 (cont)

Page 9

Tuesday, July 02, 2002 2:11 PM
pLNHiv-YFP Map.MPD (1 > 7121) Site and Sequence



Tuesday, July 02, 2002 2:11 PM
pLNHiv-YFP Map.MPD (1 > 7121) Site and Sequence

CCTATCTCAGCGATCTGTCTATTTTCGTTTCATCCATAGTTGCCTGACTCCCCGTCGTGTAGATAACTACGATACGGGAGGG
6160
GGATAGAGTCGCTAGACAGATAAAGCAAGTAGGTATCAACGGACTGAGGGGCAGCACATCTATTGATGCTATGCCCTCCC
Gly Ile Glu Ala Ile Gln Arg Asn Arg Glu Asp Met Thr Ala Gln Ser Gly Thr Thr Tyr Ile Val Val Ile Arg Ser Pro
AMP

CTTACCATCTGGCCCCAGTGCTGCAATGATACCGCGAGACCCACGCTACCGGCTCCAGATTTATCAGCAATAAACCAGC
6240
GAATGGTAGACCGGGGTCACGACGTTACTATGGCGCTCTGGGTGCGAGTGCCGAGGTCTAAATAGTCGTTATTTGGTGC
Lys Gly Asp Pro Gly Leu Ala Ala Ile Ile Gly Arg Ser Gly Arg Glu Gly Ala Gly Ser Lys Asp Ala Ile Phe Trp Gly
AMP

CAGCCGGAAGGGCCGAGCGCAGAAGTGGTCCTGCAACTTTATCCGCCTCCATCCAGTCTATTAATTGTTGCCGGGAAGCT
6320
GTCGGCCTTCCCGGCTCGCGTCTTACCAGGACGTTGAAATAGCGGAGGTAGGTACAGATAATTAACAACGGCCCTTCGA
Ala Pro Leu Ala Ser Arg Leu Leu Pro Gly Ala Val Lys Asp Ala Glu Met Trp Asp Ile Leu Gln Gln Arg Ser Ala
AMP

FspI PstI
AGAGTAAGTAGTTCCGCGAGTTAATAGTTTGCACGACGTTGTTGCCATTGCTGCAGGCATCGTGGTGTACGCTCGTCGTT
6400
TCTCATTTCATCAAGCGGTCAATTATCAAACGCGTTGCAACAACGGTAACGACGTCCGTAGCACACAGTGCAGAGCAGCAA
Leu Thr Leu Leu Glu Gly Thr Leu Leu Lys Arg Leu Thr Thr Ala Met Ala Ala Pro Met Thr Thr Asp Arg Glu Asp Asn
AMP

TGGTATGGCTTCATTACGCTCCGGTTCCCAACGATCAAGGCGAGTTACATGATCCCCCATGTTGTGCAAAAAAGCGGTTA
6480
ACCATACCGAAGTAAGTCGAGGCCAAGGGTTGCTAGTTCCGCTCAATGTACTAGGGGGTACAACACGTTTTTTTCGCCAAT
Pro Ile Ala Glu Asn Leu Glu Pro Glu Trp Arg Asp Leu Arg Thr Val His Asp Gly Met Asn His Leu Phe Ala Thr Leu
AMP

PvuI
GCTCCTTCGGTCTCCGATCGTTGTCAGAAGTAAGTTGGCCGCGAGTGTATCACTCATGGTTATGGCAGCACTGCATAAT
6560
CGAGGAAGCCAGGAGGCTAGCAACAGTCTTTCATTCAACCGGCGTCACAATAGTGAGTACCAATACCGTCGTGACGTATTA
Glu Lys Pro Gly Gly Ile Thr Thr Leu Leu Leu Asn Ala Ala Thr Asn Asp Ser Met Thr Ile Ala Ala Ser Cys Leu
AMP

TCTCTTACTGTCATGCCATCCGTAAGATGCTTTTCTGTGACTGGTGAGTACTCAACCAAGTCATTCTGAGAATAGTGTAT
6640
AGAGAATGACAGTACGGTAGGCATTCTACGAAAAGACACTGACCACTCATGAGTTGGTTTCAGTAAGACTCTTATCACATA
Glu Arg Val Thr Met Gly Asp Thr Leu His Lys Glu Thr Val Pro Ser Tyr Glu Val Leu Asp Asn Gln Ser Tyr His Ile
AMP

DraI
GCGGCGACCGAGTTGCTCTTGCCCGGCGTCAACACGGGATAATACCGCGCCACATAGCAGAACTTTAAAAGTGCTCATCA
6720
CGCCGCTGGCTCAACGAGAACGGGCGCAGTTGTGCCCTATTATGGCGCGGTGTATCGTCTTGAAATTTTCACGAGTAGT
Arg Arg Gly Leu Gln Glu Gln Gly Ala Asp Val Arg Ser Leu Val Ala Gly Cys Leu Leu Val Lys Phe Thr Ser Met Met
AMP

FIG. 16 (cont)

Tuesday, July 02, 2002 2:11 PM
pLNHiv-YFP Map.MPD (1 > 7121) Site and Sequence

Page 11

TTGGAACCGTTCTTCGGGGCGAAACCTCTCAAGGATCTTACCGCTGTTGAGATCCAGTTCGATGTAACCCACTCGTGCA
AACCTTTTGCAAGAAGCCCCGCTTTTGAGAGTTCTTAGAATGGCGACAACCTTAGGTCAAGCTACATTGGGTGAGCACGT
Pro Phe Arg Glu Glu Pro Arg Phe Ser Glu Leu Ile Lys Gly Ser Asn Leu Asp Leu Glu Ile Tyr Gly Val Arg Ala
AMP

CCCAACTGATCTTCAGCATCTTTTACTTTTACCAGCGTTTCTGGGTGAGCAAAACAGGAAGGCAAAATGCCGCAAAAAA
GGGTTGACTAGAAGTCGTAGAAAATGAAAGTGGTCGAAAGACCCACTCGTTTTTGTCTTCCGTTTTACGGCGTTTTTT
Gly Leu Gln Asp Glu Ala Asp Lys Val Lys Val Leu Thr Glu Pro His Ala Phe Val Pro Leu Cys Phe Ala Ala Phe Phe
AMP

GGGAATAAGGGCGACACGGAATGTTGAATACTCATCTCTTCCTTTTCAATATTATTGAAGCATTATCAGGGTTATT
CCCTTATTCGGCTGTGCCTTTACAACCTATGAGTATGAGAAGGAAAAAGTTATAATACTTCGTAAATAGTCCCAATAA
Pro Ile Leu Ala Val Arg Phe His Gln Ile Ser Met
AMP

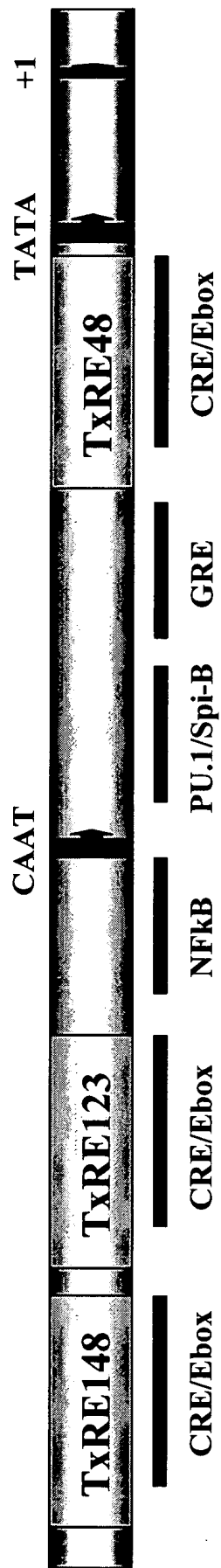
BspHI

GTCTCATGAGCGGATACATATTTGAATGTATTTAGAAAAATAAACAAATAGGGGTTCCGCGCACATTTCCCCGAAAAGTG
CAGAGTACTCGCCTATGTATAAACTTACATAAATCTTTTTATTTGTTTATCCCCAAGGCGCGTGTAAGGGGCTTTTCAC

BspHI

CCACCTGACGTCTAAGAAACCATTATTATCATGACATTAACCTATAAAAAATAGGCGTATCACGAGGCCCTTTTCGTCTTCA
GGTGGACTGCAGATTCTTTGGTAATAATAGTACTGTAATTGGATATTTTATCCGCATAGTGCTCCGGGAAAGCAGAAGT

A
> 7121
T



BLV promoter

FIG. 17

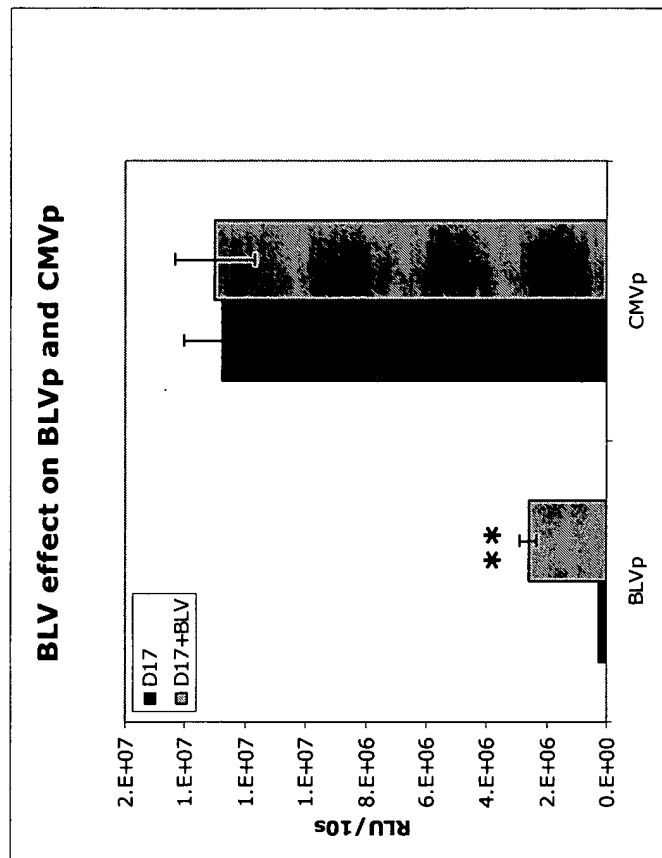


FIG. 19

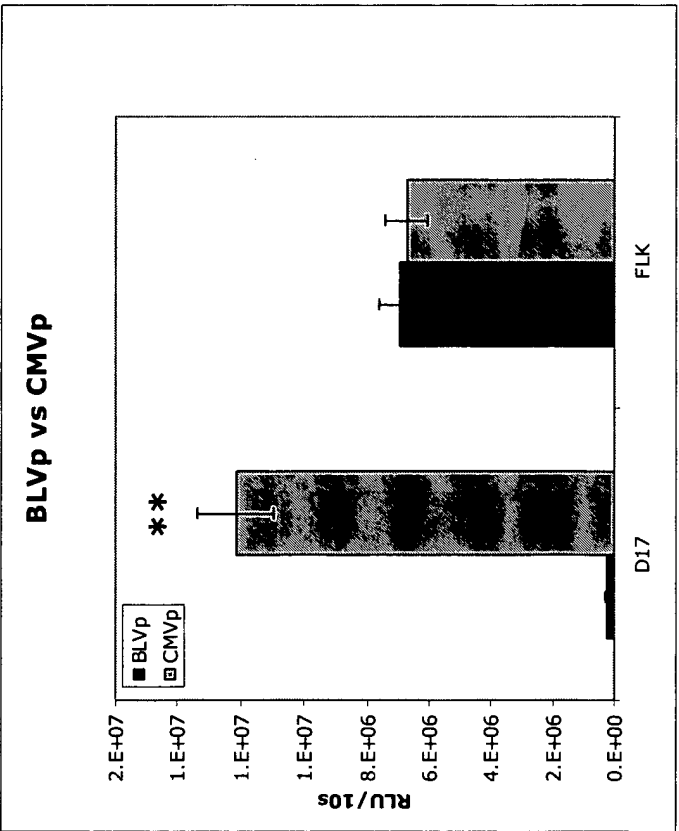


FIG. 18A

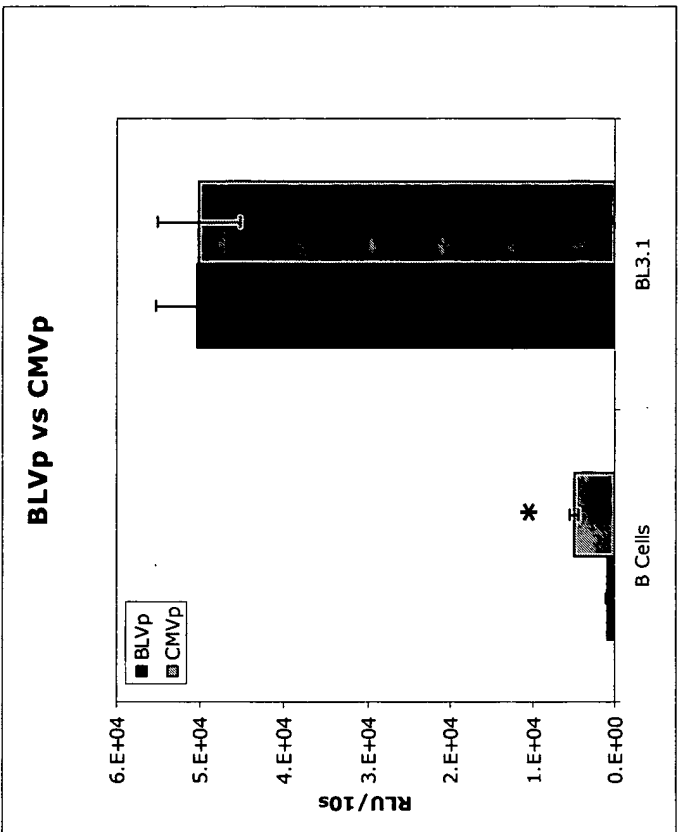


FIG. 18B

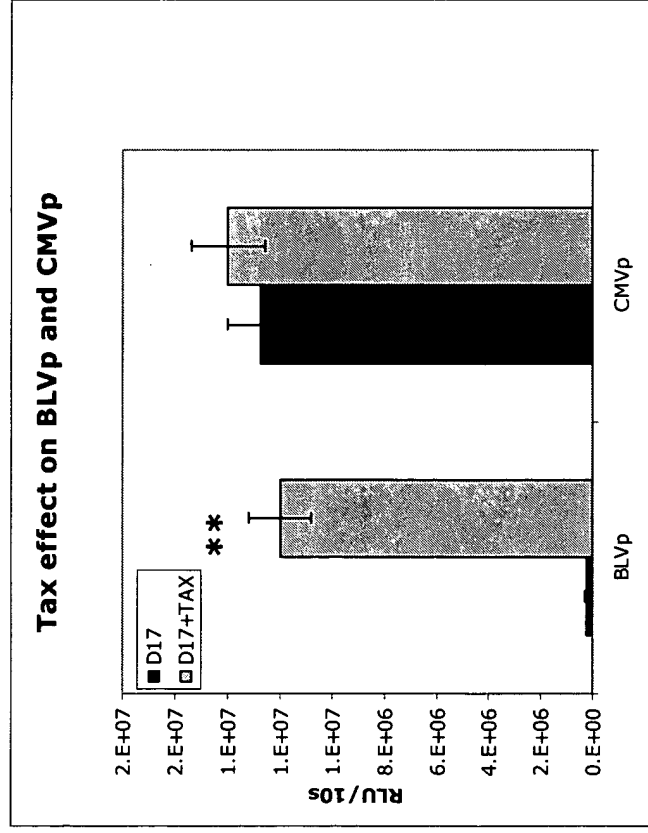


FIG. 20A

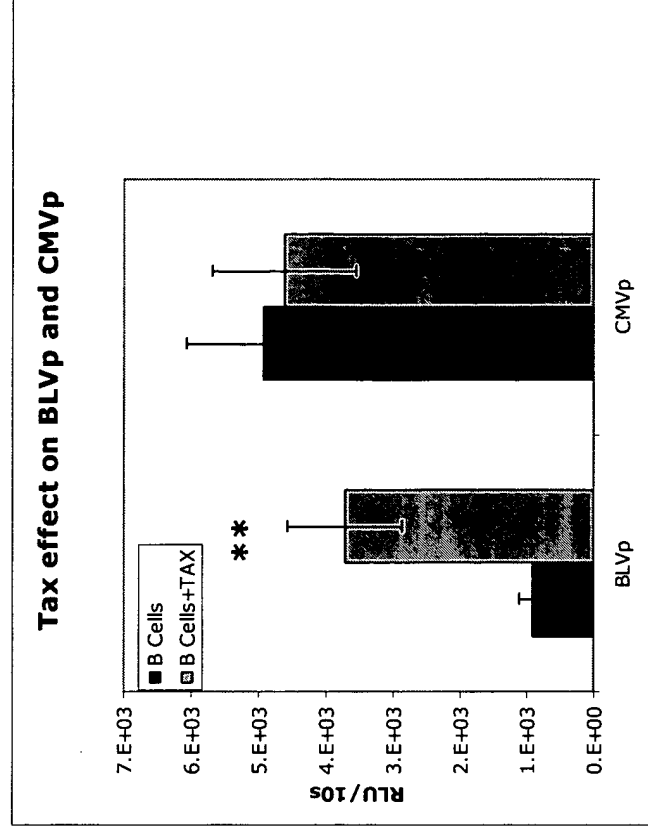


FIG. 20B